

#### Search Results -

Search Results -	7
Term	Documents
Term	474
TTR.USPT.	14
TTRS.USPT.	40068
PROMOTER.USPT.	
PROMOTERS.USPT.	31139
((TTR ADJ PROMOTER) AND 1).USPT.	2
((TTK ADJ PROMOTER) AND 1).001 1	

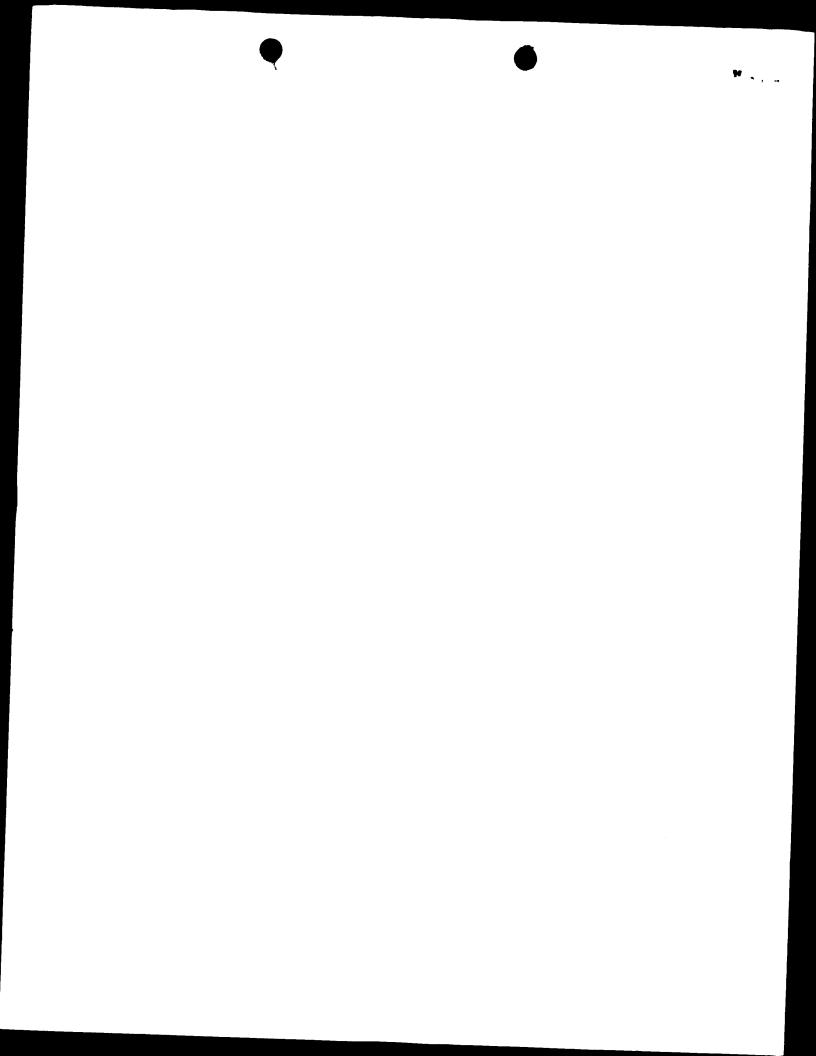
#### US Patents Full-Text Database

US Pre-Grant Publication Full-Text Database JPO Abstracts Database **EPO Abstracts Database Derwent World Patents Index** 

Data	base: IBM Ted	chnical Disclosure Bulletins	ব	
		11 and ttr promoter		Clear
R	efine Search:			

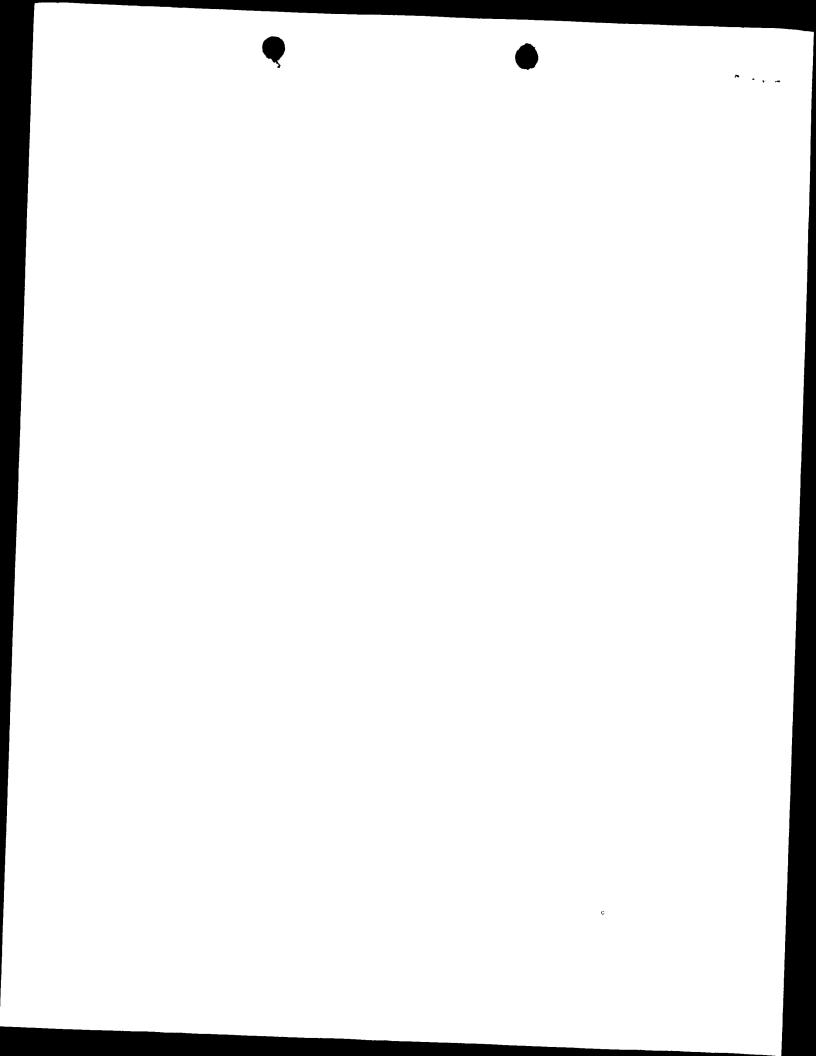
**Search History** 

**Today's Date: 1/9/2002** 





nn N	Query	Hit Count S	et Name
DB Name	11 and ttr promoter	2	<u>L13</u>
USPT		0	L12
USPT	11 and transthretin gene promoter	2	<u>L11</u>
USPT	11 and hnf 3 albumin promoter		<del>-</del>
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USF 1,1 OI D,31 1 D,22 1 D VPI	14 and junction	15	<u>L5</u>
USPT,PGPB,JPAB,EPAB,DWPI		23	<u>L4</u>
USPT,PGPB,JPAB,EPAB,DWPI	13 and heavy chain and 12	82	<u>L3</u>
USPT,PGPB,JPAB,EPAB,DWPI	12 and factor VIII	n 903	L2
LISPT PGPB, JPAB, EPAB, DWPI	11 and pharmaceutical composition		
USPT,PGPB,JPAB,EPAB,DWPI	adeno associated virus or aav	2336	<u>L1</u>
ODI 131 OL 23-1-1-7			



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OM nucleic - nucleic search, using sw model
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AR138377
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                                                                                                                 Sequence 13 from patent US 6200560.
AR138377
                                                                                                         AR138377.1 GI:14480722
                                                1 (bases 1 to 11933).
Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated virus vectors for expression of factor VIII by
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M38294 Bacteriopha

M38285 Bacteriopha

X60309 Coliphage H

AF069308 Bacteriop

AF335538 Bacteriop

AF01580 Bacteriop

AJ011580 Bacteriop

AD015492 Escherich
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AC009667 Homo sapi
AE005288 Escherich
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AR146887 Sequence
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166494 Sequence 14

L16621 Caenorhabdi

AC092343 Homo sapi

AX024319 Sequence

AX024212 Sequence

AF023164 Zea mays

AC002376 Sequence

AL157390 Homo sapi

AL591134 Homo sapi

AL160060 Human DNA
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D90798 E.coli geno
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AP002523 Oryza sat
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Best Local Similarity 100.0%; Score 934; DB 6; Length 11933;
Matches 934; Conservative 0; Mismatches 0; Indels 0; Gaps
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REFERENCE AUTHORS TITLE  JOURNAL FEATURES SOURCE BASE COUNT ORIGIN  Query Match Best Local Matches 93  Qy 1 ana Db 11060 AAAG Qy 61 ana Db 11120 TGGG QY 121 tggg Db 11180 TTCCC QY 301 CGTTA Db 11300 CGTTA CY 301 CGTGGC QY 421 gtagta Db 11300 GTCAAA QY 421 gtagta Db 11420 GTGGGCA QY 481 gtcana Db 11480 GTCAAA QY 481 gtcana Db 11480 GTCAAA QY 481 gtcana Db 11480 GTCAAA QY 541 gtggca Db 11480 GTCAAA QY 541 gtggca Db 11480 GTCAAA QY 661 ttggg Db 11540 TTGGGCAA QY 661 ttggg Db 11600 TTGGGCAA QY 661 ttggg Db 11600 TTGGGCAA QY 661 ttggg Db 11600 TTGGGGCAA QY 661 ttgggta Db 11600 TTGGGGTAA QY 661 TTGGGGTAA QY 721 tgaatag QY 721 tgaatag QY 721 tgaatag	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
Courbo, L.B., Colosi, P.C. and Olan, X. Adeno-associated vectors for expression of factor VIII Patent: US 6221349-A 13 24-APR-2001; 1. 1933 3258 a 2818 c 2717 g 3140 t    Location/Qualifiers	AR146887 11933 bp DNA Sequence 13 from patent US 6221349. PAT 08- AR146887 AR146887.1 GI:15110690 Unknown. Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
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                                                                            /note="EcoRI site normally present at the 3' end of lacZ has been temoved by an uncharacterized mutation"
/translation="VVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLR
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                                                                   /codon_start=1
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39091 AAACGCCAGGAGGTTGTTAGCGCGACCTCCTGCCACCCGCTTTCACGAAGGTCATGTGTA 39032
                                                                                                                                                                                                                                                                                                                                                              38971 TGGGTTGTGCTGTGGGGGGGGGGGGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 38912
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                                                    121 tgggttgtgctgttgctgggcggcgatqacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                   241 tottcacgattatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 aaacqqcaqqaqqttqttaqcqcqacctcctqccacccqctttcacqaaqqtcatqtqta 60
361 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                               TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 38792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.8%; Score 923.2; DB 12; Length 42529; Similarity 99.7%; Pred. No. 4.4e-283;
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PPTVPTENPTGCYSLTFNVDESWLQBGQTRIIFDGYNSAFHLWCNGRWVGYGDDSRLP
PPTVPTENPTGCYSLTFNVDESWLQBGQTRIIFDGYNSAFHLWCNGRWVGYGDSSLP
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VATRENDDFSRAVLEAEVQWGCBELRDYLRVTYSLWGGETQVASGTAPFGGEIIDERGE
VATRENDDFSRAVLEAEVQWGCBELRDYLRVTYSLWGGETQVASGTAPFGGEIIDERGLL
YADRWTLRLWVENPKLWSAEIPNLYRAVVELHTPADGTILEMEADVGCSTYPNHPLWT
LLNGKPLLIFGQVNREHHPLHGQVMDEQTMVODILLMKONNENAVRGSHYPNHPLWT
LCDRYGLYVVDEANIETHGQVMRKLTDDPRWLPAMSERVTBWQDRDRNHFSVIIWSL
LCDRYGLYVVDEANIETHGAVPMNRLTDDPRWLPAMSERVTBWQDRDRNHFSVIIWSL
GNESGHGANHDALYRWIKSVDPSREVQXEGGGADTTATDIICPMYARVDEDQPFPANP
GNESGHGANHDALYRWIKSVDPSREVQXEGGGADTTATDIICPMYARVDEDQPFPANP
GNESGHGANHDALYRWIKSVDPSREVQXEGGGADTTATDIICPMYARVDEDQPFPANP
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KWSIKKWLSLDGETRPLIICEYAHAMONSLGGFAKYWQAFRQYPRLAKHQQOFFQFRLS
LIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLYFADRTPHPALTEAKHQQOFFQFRLS
LIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLYFADRAFQGKQLIELPELPQPES
GQTIEVTSEYLFRHSDNELLHWMYALDGKPLASGEVPLDVAPQGKQLIELPELPQPES
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SDMYTPYVFPSENGLRCGTELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLLHAEE
GTWLNIDGFHMGIGGDDSWSPSYSAEFQLSAGRYHYQLVWCQK"
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AGOLMITVRVVOPNATAMSEAGHISAMOOWRLAENLSVTLPAASHAIPHLTTSEMDFC
TELGNKRWOFNROSGFLSOMWIGHKOLLTPLROOFFRAPLDNDIGVSEATRIDPNAW
TELGNKRWOFNROSGFLSOMWIGHKOLTTTAHAWOHOGKTLFISRKTYRIDGSGOM
VERWKAAGHYQAEAALLOCTADTLADDVLITTAHAWOHOGKTLFISRKTYRIDGSGOM
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24475. .25665
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YGVLLALYALMOFLCAPVLGALSDRFGRRPVLLASLLGAT DYA HATTPVLWITLYAG
RIVAGTTGATGAVAGAY IAD ITDGEDHARHFGLMSACFGVGMVAGPVAGGLLGALSLL
RIVAGTTGATGAVAGAY IAD ITDGEDHARHFGLLSLASACFGVGMVAGAMT IVAALMTV
APFILAAAVLMGLUNLLGGELMAGESHKGERRPMPLRARNHVSSFRAMAGAMT IVAALMTV
FEIMQLVGQVPAALMVLTGEDBRFRWSATMIGLSLAVGGIGMPALQAMLSRQVDDDHQG
KQAIIAGMADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
KQAIIAGMADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
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33602. .35450
/note="imm21 substitution"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38491 TTTGTGGCATTGCACCACAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 38432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 gtagtaagcgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                         Submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                     artificial sequence; vectors.

1 (bases 1 to 42530)
St Pierre, R. and Linn, T.

A refined vector system for the in vitro construction of
                                                                                                                                                                                                                      StPierre, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                            Single-copy transcriptional or translational fusions to lacz
                                                                                                                                                                                                                                                                                                                                                    Cloning vector TLF97-2. Cloning vector TLF97-2.
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Cloning vector TLF97-2,
                                                                                                                                                                                                                                                                                                                                                                                                                          vector, complete sequence
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                /gene="lacy" .20760)
                                                   complement(19507. .20760)
                                                                    complement(19404. 19489)
/note="rrnBT2 terminator"
                                                                                          /organism="Cloning vector TLF97-2"
/db_xref="taxon:43841"
                                              /gene="lacy"
codon_start=1
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1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
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/note="imm21 substitution"
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/product="mailine statement of tetracycline resistance protein statement of te
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KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
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/note="multiple cloning site"
complement(23974. .24142)
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                                                                                                                                98.8%; Score 923.2; DB 12; 99.7%; Pred. No. 4.4e-283; A. Mismatches 3;
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/product="lactose permease"
/protein_id="AAC5351.1"
/db_xref="GI:1066309"
/taaslation="MYYLKNTNFWMFGLEFEFFYEFIMGAYFPFFPIWLHDINHISKSD TITETESLESULFQPLEGLLSDKLGLRKYLLWIITGMLYWFAFFFIFTFGPLLOYN MFTINNOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFAKTDAPSSATYANAVGANHSAFSUKLALELFG NATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILFAKTDAPSTATTONOFYFWLGSGCALILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPSTATTONOFYFWLGSGCALILAVILFAKTDAPST
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FFAPLIINRIGGKNALLLAGTINSVRIIGSSFATSALEVVILKTLHMFEVPFLLVGCF
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                                                                                                                                                                                                                                          DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38972 TGGGTTGTGCTGTGCTGGGCGGCGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 38913
                                                                                                                                                                                                                Вp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38852 TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCCGAAAC 38793
                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38732 TCTGCCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCG 38673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 tgggttgtgctgttgctgggggggggtgacgcctgtacgcatttggtgatccggttcttgc 180
KEYWORDS
SOURCE
                                                                             RESULT 5
CVU39286/c
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                                ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 tottcacgattatcgactcaatgotottacctgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 totgootgogatggttggagttocagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                      38432 TTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATATGCTGCGCTTGCTGGCATCCT 38373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 gtagtaagcgccgcctctttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                                                                                                                                           38372 TGAATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTCCCCCACAGCTC 38313
                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 gtcaaatttacccaattttaftcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                               38312 TGTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAATCTCTGCATCTTGCCCCGG 38253
                                                                                                                                                                  38252 CGTCGCGGCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACTTGCAGTACCTT 38193
                                                                                                                                                                                                                                                                                                                                                   38192 TGCCTTAGTATTTCCTTCAAGCTTTGCC 38165
                                                                                                                                                                                                                                                                                                                   661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                      721 tgaatagocgacgcotttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                             781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 840
                                                                                                                                                                                  841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttcoggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                             901 tyccttagtatttccttcaagctgcccc 928
                                                      CVU39286 42531 bp
Cloning vector TLF97-3,
  Cloning vector TLF97-3.
                         U39286.1 GI:1066312
                                             vector, complete sequence
                                                                               DNA
                                                                 phage lambda lacZ translational fusion
                                                                                         13-APR-1996
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REFERENCE
AUTHORS
TITLE
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A refined vector system for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single-copy transcriptional or translational fusions to lacz gene 169 (1), 65-68 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada University of Western Ontario, London, Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 42531)
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/translation="VVLORRDWENDGUTQLINRLAAHPPFASWRNSEEARTDRPSQQLR
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SEDLSAFLRASGURLAVWVLRWSDOSYLEDODWRRWSGI FRDVSLIHKPTQLSDFH

SEPDLSAFLRASGURLAVWVLRWSDOSYLEDODWRRWSGI FRDVSLIHKPTQLSDFH

VATRENDDFSRAVLEAFVQMCGELROYLRTVSLWGGETQVASGTAPFGGEI I DERGG

SEPDLSAFLRASGURHEHPLHGOVMDEQTWVQDILLHKQNNFNAVRCSHY PHHPLWFI

LINGKPLLIRGYWRHEHHPLHGOVMDEQTWVQDILLHKQNNFNAVRCSHY PHHPLWFI

LANGKPLLIRGYWRHEHHPLHGOVMDEQTWVQDILLHKQNNFNAVRDDENDFSVIIWSL

LINGKPLLIRGYWRHEHPLHGOVMDEQTWVQDILLHAVORDRWHPSVIIWSL

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GONESGHGANHDALYRWIKSVDPSRAVYOYEGGADTTNATDI ICPMYARVDENDGPFORRUS

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SUNGSGHGANHDALYRWIKSVDPSRAVYOYEGGADTTNATDI ICPMYARVDENDFC

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LIKYDENGNWSANGGDFSOTFNDROFCMNGIVFAADRPPHPALTEAKTDENDFC

GQTITUTSEYLFHSDNELLHWAYALDGKPLASGEVVLDVAPOGKOLLTELPELPOPES

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AGOLWLTVRKVQPNATAWSEAGHTSAWQOWRLAENVMLGLGPOENVPRLTAACFBRWDLPL

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SDMYTPOYOFDSENGLGGTRELNYGPHOWREDFOENISKYSGOGN

GTWLNIDGEHMGIGGDDSWSPSVSAEFOLSAGRYHYQLVWCOK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="rrnBT2 terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:43842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Cloning_vector TLF97-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="lacy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="beta-galactosidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          has been removed by an uncharacterized mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="lac2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="EcoRI site normally present at the 3' end of lacz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                  /note="multiple cloning site" complement(23975...24143)
                                                                                                                                                                    complement(23876.
                                             /note="rrnBT1 terminator"
24477. .25667
/gene="tetR"
/gene="tetR"
                                  . 25667
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38433 TTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGGGATATGCTGCGGCTTGCTGGCATCCT 38374
                                                                                                                38493 TTTGTGGCATTGCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 38434
                                                                                                                                                                                38553 GTGGCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTC 38494
721 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                  38613 GTCAAATTTACCCCAATTTTATTCAATAAGTCAATATCATGCCGTTAATATGTTGCCATCC 38554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                 38673 GTAGTAAGGGCGCCCTCTTTTCATCTCACTACCACAAGGAGGGAATTAACCCATCGTTGA 38614
                                                                     661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                 38733 TCTGCCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCG 38674
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38793 CGTTATGCAGGCTCTAACTATTACCTGCGAACTGTTTCGGGATTGCATTTTGCAGACCTC 38734
                                                                                                                                                                                                  541 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38853 TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 38794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38913 TTCCGGTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAGGCTCGCCGAC 38854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 925;
                                                                                                                                                                                                                                                                                                                                   421 gtagtaagcgccgcctotbttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38973 TGGGTTGTGCTGTGCTGGGGCGGCGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 38914
                                                                                                                                                                                                                                                                                                                                                                                                   361 totgootgogatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 tottoacgattatogactcaatgotottacotgttgtgcagatataaaaaatcocgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                    tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
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10292 a 10534 c 11615 g 10082 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="netracycline resistance protein"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.8%; Score 923.2; DB 12; 99.7%; Pred. No. 4.4e-283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38253 CGTCGCGGCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACTTGCAGTACCTT 38194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38313 TGTTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAATCTCTGCATCTTGCCCCCGG 38254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38373 TGAATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTCCCCCCACAGCTC 38314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901 tyccttagtatttccttcaagctgcccc 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-SBP-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 42704)
StPierre,R. and Linn,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning vector lambda TXF97.
Cloning vector lambda TXF97
artificial sequence; vectors.

1 (bases 1 to 42704)
St Pierre, R. and Linn, T.
A refined vector system for the in vitro construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single-copy transcriptional or translational fusions to lacz gene 169 (1), 65-68 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVU37692 42704 bp DNA SYN 13-APR-1996 Cloning vector lambda TXF97, lacZ transcriptional fusion vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U37692.1 GI:1051181
                                                                                                /note="EcoRI site normally present at the end of lacz has been removed by an uncharacterized mutation"
                                                  Complement(20812. .23886)
/gene="lacz"
                                                                                  /gene="lacz"
                                                                                        TLISVFTLSGPGPLSLLRRQVNEVA" complement(20812. 23886)
                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                               removed by an uncharacterized mutation complement(19404. 19489)
/note="rrnBrz_terminator"
                                                                                                                                                                                                                                                                                                            complement(19507. .20760)
                                                                                                                                                                                                                                                                                                       /gene="lacy"
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                                                                                                                                                                                                                                                                                                                                                                                 /note="BamHI site normally present at this site has been
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/db_xref="taxon:43300"
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BASE COUNT
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Best Local Similarity 99.7%;
Matches 925; Conservative
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/translation="MTMITDSLAVYLQRRDWENPGVTQLNRLAAHPPFASWRNSEEAR
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/note="multiple cloning 24316)
complement(24148. 24316)
/note="trhBT1 terminator"
24650. 25840
/gene="tetk"
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//translation="MKSUNALIVILGTVTLDAVGIGLVMPVLPGLLRATTPVLMILYAG
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RYVAGITGATGAVAGAYIADITDGEDRARHFGLMSAQFTGVGWALMTV
APPLAANVLNGLMLLLGCFLMOESHKGERPMPLRARHVSSFRWARGMTIVAALMTV
APPLAANVLNGLMLLTGETLMOESHKGERPMPLARHFGLHALADAKISRGVDDDDGG
FINOLVGGVPAALMVTFGEDRFRWAAFPIMILLASGGIGMPALOAMISRGVDDDDGG
KQAIIAGMAADALGYVLLAFATGGWMAAFPIMILLASGGIGMPALOAMIYCLAALYLVCLPALRRGAWSR
QLQGSLAALTSLTSLTGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAWSR
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/protein_id="AAC53647.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 cgftatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
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                             PUBMED
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                                                                                                                                                                                                                                                                                                                                              901 tgccttagtatttccttcaagctgcccc 928
                                                                                                                                                                                                         48502 bp DNA circl
Bacteriophage lambda, complete gent
J02459 M17233 W24325 V00636 X00906
J02459.1 GI:215104
                                                                                                                                                                                    DNA-binding protein; circular; coat protein; complete genome; origin of replication; repressor; unidentified reading frame.
                                                     Lebowitz, P., Weissman, S.M. and Radding, C.M.
Nucleotide sequence of a ribonucleic acid transcribed in vitro from lambda phage deoxyribonucleic acid lambda phage deoxyribonucleic acid transcribed journal of biological chemistry. 246 (16), 5120-5139 (1971)
                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Talled phages; Siphoviridae;
                                                                                                                                                                      bacteriophage lambda.
                                                                                                                                                                                 origin of replication; repressor;
                                                                                                                Lambda phage group.
1 (bases 44588 to 44780)
   Wu, R. and Taylor, E.
                                4936723
                                              71288594
                (bases 1 to 12)
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Proceedings of the National Academy of Sciences of the United States of America. 73 (3), 712-716 (1976)
                                    Deletions of lambda phage locating a prm mutation within the rightward operator
                                                                                         12 (bases 37946 to 38039)
Smith, G.R., Eisen, H., Rei
                                                                                                                                       958438
                                                                                                                                                                                                                                              Determination of genes, restriction sites, and DNA sequences surrounding the 6S RNA template of bacteriophage lambda Proceedings of the National Academy of Sciences of the United 75,17847
                                                                                                                                                                                                                   Walz
                                                                                                                                           Lambda repressor regulates the switch between PR and Prm promoters
                                                                                                                                                                                                                                                                                                                                                                                            Maniatis,T., Jeffrey,A. and Kleid,D.G.
Nucleotide sequence of the rightward operator of phage lambda
Proceedings of the National Academy of Sciences of the United
States of America. 72 (3), 1184-1188 (1975)
                                                                                                                                                                                                                                                                                                                                            10 (bases 44588 to 44773)
Sklar, J., Yot, P. and Weis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahlberg, J.E. and Blattner, F.R. Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda Nucleic acids research. 2 (9), 1441-1458 (1975)
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Kleid,D.G., Agarwal,K.L. and Khorana,H.G.
The nucleotide sequence in the promoter region of the gene N in
bacteriophage lambda
                                                                                                                                                                                            (bases 37905 to 37989)
lz.,A., Pirrotta,V. and Ineichen,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Academic Press, New York (1973)
6 (bases 37945 to 38027)
Maniatis T., Ptashne M., Backman K., Kield, D., Flashman, S.,
Jeffrey, A. and Maurer, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and regulatory sites
(in) Fox,C.F. and Robinson,W.S. (Eds.);
VIRUS RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544;
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In vitro transcription products of lambda DNA: Nucleotide sequences
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Amino acid sequence of lambda phage endolysin
Nature New Biol. 233, 230-231 (1971)
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24 (bases 37938 to 38016; 35589 to 35666)
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                                                               178. Nucleotide sequence surrounding the cos site of bacteriophage
                                                                                              23 (bases 13 to 72; 48391 to 48502) Nichols, B.P. and Donelson, J.E.
                                                                                                                                                 Adhya, S. and Gottesman, M.
Control of transcription termination
Annual review of biochemistry. 47, 967-996 (1978)
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Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and
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Davies, R.W., Schreier, P.H. and Buchel, D.E.
Nucleotide sequence of the attachment site of coliphage lambda
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Roberts, T.M., Shimatake, H., Brady, C. and Rosenberg, M.
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DNA base sequence of the po promoter region of phage lamdba
Paranana 265 (5590), 117-121 (1977)
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Plashne,M., Backman,K., Humayun,M.Z., Jeffrey,A., Maurer,R.,
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Science, 194 (4261), 156-161 (1976)
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Nucleotide sequence of cro, cII and
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Cloning vector lambda
U02453
                                                                                    Submitted (07-007-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA 1020 East Meadow Circle, Palo Alto, CA 94303, USA This sequence has been compiled from information in the sequence databases, published literature and other sources. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECHGCLONTECH.COM.
                                                                                                                                                                                                                                                                              Frischauf,A.M., Lehrach,H., Poustka,A. and Murray,N. Lambda replacement vectors carrying polylinker sequences J. Mol. Biol. 170 (4), 827-842 (1983)
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/organism="Cloning vector lambda
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Matches 924; Best Local Similarity

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                                                                                                                                                                                                                                                                            tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg
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                                    TTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 5108
                                                           tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                          GTGGCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTC
                                                                                                                                                                               GTCAAATTTACCCAATTTTATTCAATAAGTCAATATCATGCCGTTAATATGTTGCCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Cirlce, Palo Alto, CA 94303, USA
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306 tgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctctctgc 365
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Bacteriophage lambda late transcription promoter region DNA
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                                                                                                                                                                  GTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAAGCTCGCCGACTCTTC 557
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/db_xref="taxon:10710"
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bacteriophage lambda
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                                                                                                                                                                                              /transI_table=11
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PYADYCRSGATPQARCRDCHGTGRAVDIAKTHAGETTANNTTNATTD"
                                                                                                                                                                                                                                                                                                                  /organism="bacteriophage lambda"
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                                                                                                                                                                                YRAVTMLIPNLTOPTWSRTVKPLYDALVVOCHKEESIADNILNAITR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-SEP-1991) B.L. Atkinson, Columbia Univ College of Physicians and Surgeons, 701 West 168th Street, New York NY 10032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteria phage HK022.
Enterobacteria phage HK022
Enterobacteria phage HK022
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 gcttaacagtgcgtgaccaggtgggttgggtaaggtttgggattagcatcgtcacagcgc 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 aaatgttgtctgcgattgactcttctttgtggcattgcaccaccagagcgtcatacagcg 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 TCATGCCGTTAATATGTTGCCATCCGTGGCAATCATGCTGCTAACGTGCGACCGCATTCA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 tcatgocgttaatatgttgocatccgtggcaatcatgotgotaacgtgtgaccgcattca 575
                                                                            Submitted (31-MAY-1998) Pittsburgh Bacteriophage Institute & Dept. of Biological Sciences, University of Pittsburgh, Pittsburgh, PA
                                                                                                                                 Direct Submission
                                                                                                                                                                                                        Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages
J. Mol. Biol. 299 (1), 27-51 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                        2 (bases 1 to 40751)
Juhala,R., Ford,M.E., Duda,R.L., Youlton,A., Hatfull,G.F. and
                                                                                                                                                                                                     10860721
                                                                                                                                                                                                                                                                 Lambda phage group.

(bases 1 to 40751)

Juhala,R.J., Ford,M.E., Duda,R.L., Youlton,A., Hatfull,G.F. and
                                                                                                                                                                                                                                                                                                              Enterobacteria phage HK022.
Enterobacteria phage HK022
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                 AF069308.1 GI:6863111
                                                                                                                                                                                                                                                                                                                                                                                                                         AF069308 40751 bp DNA
Bacteriophage HK022, complete genome.
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/db_xref="taxon:10742"
                        ∕organism="Enterobacteria phage HK022"
                                                               Location/Qualifiers
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185 c 216 g
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95.18;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542.
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DQFRKDADAIGLSLPLVEFGQGFKDMGPAVDTLESLMLNGRVRHGMHPVLTMCAVNAV
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DAEMMASRKFOVSELARETGVPPHLVGJVEKSTSWGSGIEOQNLGFLQYTLOPYISRW
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5219...5545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="gp10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MIAPIFSVCASSPEVTDLLGSNPVRIYPEGIQDDNVVYPYVVWQ
NITGSPENYIAQRPDADFFTLQVDAYADTVDEVIAVATALRDAIEPHAHITRWGGQER
DPETKRYRYSFDVDWIVTR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGKAIDRAIRLAMKKGTTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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PTAAENGASGAVDGLVLPDSRTWFVFKGYVSDFPFDFSANTVVSTSASIQRSGSAVWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                     /codon_start=1
                                                                                                                                                                                                                                           PKVVTP"
                                                                                                                                     /note="gp13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 5975
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                                                                                                                                                                                                .8282
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KEYWORDS
                                                                                                     VERSION
                                                                                                                       ACCESSION
                                                                                                                                            DEFINITION
                                                                                                                                                                            AF335538/c
                                                                                                                                                                                                    RESULT
                                              ORGANISM
                                                                                                                                                                                                                               36574 GGCAATCTCTGCATCTTGCGCCCGGTGTCGCGGCACTACGGCAATAATCCGCATAAGCGA 36515
                                                                                                                                                                                                                                                                                                                                                                                   36634 TCTCGACAACTCTCCCCCACTGCTCTGTTTTGGCAATATCAACGGCCCGGCCAGTACCGT 36575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            36694 GATATGCGGCGCTTGCTGGCATCCTGGAATAGCCGACGCCTTTGCATCTTCCGCCACTCTT 36635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36754 GCTTAACAGTGCGTGACCAGGTGGGTTGGGGTAAGGTTTGGGATTAGCATCGTTACAGCGC 36695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36814 AAATGTTGTCTGCGATTGACTCTTCCTTGTGGCATTGCACCACCAGAGCGTCATACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36874 TCATGCCGTTAATATGTTGCCATCCGTGGCAATCATGCTGCTAACGTGCGACCGCATTCA 36815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36934 AACGAGTGCATTTATCCATCGTTGGGTCAAATTTACCCAACTTTATTCAAAAAGTCAATA 36875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              696 gatatgctgcgcttgctggcatccttgaatagccgacgcctttgcatcttccgcactctt 755
                                                                                                                                                                                                                                                                                                                                                                                                       756 tetegacaacteteeccecacagetetgttttggcaatateaacegcacggcetgtaccat 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636 gcttaacagtgcgtgaccdggtgggttgggtaaggtttgggattagcatcgtcacagcgc 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 aaatgttgtctgcgattgactcttctttgtggcattgcaccaccagagcgtcatacagcg 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 tcatgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattca 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                              99caatctctgcatcttgcc&ccggcgtcgcggcactacggcaataatccgcataagcga 875
Viruses; dsĎNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                         AF335538.1 GI:13517559 .
                                        Bacteriophage
                                                      Bacteriophage HK620.
                                                                                                                       Bacteriophage HK620, complete genome.
                                                                                                                                                          AF335538
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                                                                                                                                                38297 bp .
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/protein_id="Analog366.1"
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RERYCSLNPMLRVEWGAGLVSSMIANVNRDFKRPPFNPTDFTLHFTKVKAADGPISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/note="gp16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="gpl4; presumed to be expressed as the downstream part of a translational frameshift product; start is placed at the presumed frameshift site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKLTLDALKESGAFTGRPVEKEITWTQGDKKTTATVYVRPMGYH
TATSDVLAFGGKVDGVAGRIAASICDEHGKPIFTPADITGEADPERGALDGGLTVALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="lambda gpG analog"
/protein_id="AAF30365.1"
/db_xref="GI:6863124"
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                                      HK620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Score 436.2; DB 7; Length 40751; 95.1%; Pred. No. 1.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                  DNA
                                                                                                                                            circular PHG
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                                                                                                                                   03-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark, A.J., Inwood, W.B., Cloutier, T. and Dhillon, T.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 38297) Clark, A.J., Inwood, W.B., Cloutier, T. and Dhillon, T.S. Nucleotide Sequence of Coliphage HK820 and the Evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambdoid Phages
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                                        complement(1664 . .1702)
/function="phage integration"
complement(1689 . .1701)
                                                                                                                                            RARWLYRDHCEFKNKLLSRANG"
/bound_moiety="cII protein"
                                                                                                                                                                    /translation="MQHELQPDSLVDLKFIMADTGFGKTFIYDRIKSGDLPKAKVIHG
                                                                                                                                                                                                                                /protein_id="AAK28851.1"
/db_xref="GI:13517562"
                                                                                                                                                                                                                                                                                                                /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1457. .1657)
/gene="hkaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="hkaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1368.
                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="attP core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1324. .1464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="integrase"
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGKIAGKIFLTSKKHHSNQSPAASSRCLQGTPFISSLQSVPVRK
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1324 . 1464)
/gene="hkaB"
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LLTTLSSITKPVSEFVFAGRNDKKKPICENAVLLVIKQIGYEGLESGHGFRHEFSTIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="attp"
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/gene="int"
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complement(join(1. 23,38289. .38297))
/note="terminator for prophage excision transcript; XIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="site-specific recombination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(50. 1207)
/gene="int"
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/db_xref="taxon:155148"
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="mnknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="hkaD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASWKPSHWMPLPEPPL"
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/gene="hkaG"
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complement(3507. .3989)
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                                                                                                                                                                                                                  complement(3986. .4150)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15617 AACGAGTGCATTTATCCATCGTTGGGTCAAATTTACCCAACTTTATTCAAAAAGTCAATA 15558
                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 tcatgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattca 575
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                                                                                                                                                                                                                                                                                                                                      636 gcttaacagtgcgtgaccaggtgggttgggtaaggtttggggattagcatcgtcacagcgc 695
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                                                                                                                         GCTTAACAGTGCGTGACCAGGTGGGTTGAGTAAGGTTTGGGATTAGCATCGTTACAGCGC 15378
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94.3%;
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Pred. No. 1.4e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-JUN-1998) Pittsburgh Bacteriophage Institute & Dept. of Biological Sciences, University of Pittsburgh, Pittsburgh, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hendrix, R.W..
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Juhala, R., Ford, M.E., Duda, R.L., Youlton, A., Hatfull, G.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic mosaicism in the lambdoid by J. Mol. Biol. 299 (1), 27-51 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage нк97.
Bacteriophage нк97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
1 (bases 1 to 39732)
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KDADISKRESWLAANPALGTERSEKDMARQAEKAGRMPSFENTFRNINLNQRVSTVSP
{	t FISRSVWELCGEMPINTPRKWYAGLDLSARNDLTALVIAGEADDGVWDVFPFFWTPQK}
                                                                                                                                                                                                                                                                                                                                   /gene="2"
542. .205
                                                                                                                                                                                                                                                                                                                                                                                                          VELQRTILAQRRDLQIHSHATNGESRDQKKRNQNDRDARNTKNEHQDQDDNLIAFPKH
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50 .53
                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                      /note="Gp2"
                                                                                                                                                                                                                                                                                                         /gene="2"
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/db_xref="taxon:37554"
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4028
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/cod~
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                    EEGOLLNGDGTGDNLEGLÑKVATAYDTSLNÄTGDŤRADIIAHAIYOVTESEFSASGIV
LNPRDWHNIALLKDNEGRYIFGGPQAFTSNIMWGLPVVPTKAQAAGTFTVGGFDNASQ
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AAMQHGTVEGMSVGFSVAKDDYTIIFTGRIFKNIQALREISVCTFFANEQAGIAANKS
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2056. .3330
/gene="3"
                                                                                                                                                                                                                                                                 /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
/product="major head subunit precursor"
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DQFRKDADAIGLSLPLVEFGQGFKDMGPAVDTLESLMLNGRVRHGMHPVLTMCAVNAV
VVKDAAGNRKLDKSKATGRIDGNVAMTMSVGAANGEVTEQGGDFDDFIFRPLSM*
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Best Local Similarity Matches 451; Conserv
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5545.
                 Conservative
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/gene="10"
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/gene="11"
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6326. 6673
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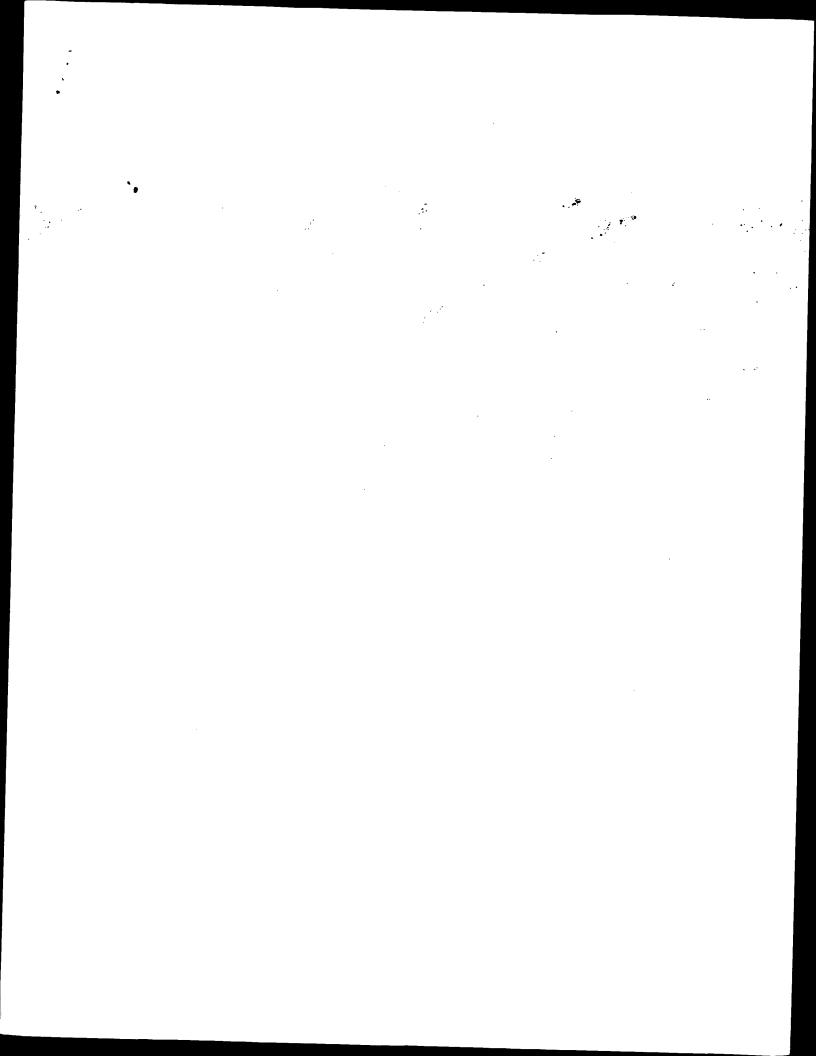
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                               6.8; DB 7;
. 1.2e-124;
tches 22;
                                                                                            Length 39732;
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35560 TGGCAATCTCTGCATCTTGCGCCCGGCGTCGCGGCACTACGGCAATAATCCGCATAAGCG 35501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 ggcttaacagtgcgtgaccaggtgggttgggtaaggtttgggattagcatcgtcacagcg 694
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Search completed: January 8, 2002, 17:22:58 Job time: 12469 sec



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934
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Copyright (c) 1993 - 2000 Compugen Ltd.
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# SUMMARIES

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A 12 12 12 11 11 11 11 11 11 11 11 11 11	Query Match Length DB
11933 11933 37,856 49617 49617 469 469 469 469 542 936	LengthroB
21 AAD00121 22 AAD08612 24 AAA11992 24 AAA11992 25 AAC37411 25 AAC37411 27 AA112811 28 AA112811 29 AA112811 20 AA113417 21 AA11383 22 AA11883 22 AA14395 22 AAF5825	<u>.</u>
AAD00121 AAD08612 AAA11992 AAA11992 AAC37411 AAF28541 AAF12818 AAF34173 AAF102735 AAF18836 AAF18836 AAF18836 AAF43958	1
	D
Human factor VIII B. Cellulosum DNA S. Cellulosum DNA Arabidopsis thalia Genomic fragment # probe #2751 for ge probe #2859 used t probe #2726 used t probe #8769 for ge probe #12644 used Oligonucleotide D1	Description
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## ALIGNMENTS

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AAD00121
                               AAD00121 standard; DNA; 11933 BP.
                                                                                                                                                                                                                            Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII; herostant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor lalpha; Erlalpha; hevili, HNF-3 albumin promoter; human elongation factor lalpha; bhuman growth hormone; hGH; inverted terminal repeat; ITR; haemophilia; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                     AAD00121;
                                                                                                                                                                                                                                                                                       Recombinant adeno associated vector construct, pAAV-F8-1.
                                                                                                                                                                                                                                                                                                              31-JUL-2000 (first entry)
                                                                                                                                                                                   WO200023116-A1.
                                                                                                                                                                                                         Adeno associated virus.
                                                                                                                                                            27-APR-2000.
                                                                                                     20-OCT-1998;
24-MAR-1999;
                                           Couto LB, Colosi PC;
                                                                  (AVIG-) AVIGEN INC.
                                                                                           30-JUL-1999;
                                                                                                                                       19-OCT-1999;
New recombinant adenovirus-associated vector, useful for gene therapy
                     WPI; 2000-339536/29.
                                                                                                        98US-0104994.
99US-0125974.
                                                                                               99US-0364862
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                                                                                                                                                                           11480 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
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                                                    541 gtggcaatcatgctgctaacgfgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                                                                                                      11300 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcatttttgcagacctc 11359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 934;
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601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                         481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                          11240 tetteaegattategaeteaatgetettaeetgttgtgeagatataaaaaateeegaaac 11299
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                                                                                                                                                                                                                                                                    361 totgootgogatggttggagttocagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11060 aaaggeegeagegtaactattaetaatgaatteaggaeagaeagtggetaeggeteagtt 11119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11000 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 11059
                                                                                                                                                                                                                                                                                                                                        301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                           241 tottoacgattatcgactcaatgotottacotgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hPVIII coding region comprises the heavy chain gene segment with the and 5 amino acids from the N-terminus of the B domain. Al and A2 domains comprises the C-terminal 85 amino acids of B domain and the A3 domain of the B domain. The light chain into the same plasmid seperated by 42 nucleotides coding for 14 residues factor VIII gene. The adeno-associated viral vectors are used for gene therapy to treat haemophilia. This method allows prolonged expression of their by because of their broad host range, safety profile and duration of expression in the infected hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-lalpha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII) is inserted between the AAV inverted terminal repeat (ITR) regions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 5; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 934; DB 21; 100.0%; Pred. No. 4.9e-312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 11933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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δÃ

Qy Db

В Qy В

В γ Вþ δÃ DЬ Qy Ъ Qy 뫄 δÃ Вþ Qγ В

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is particular humans. The rAAV vector provides high level and long term expression of biologically active clotting factor VIII in vivo. The present sequence is pAAV-F8-1 vector without the plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                 administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a
                                                                                                              The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                  Claim 18; Fig 5; 90pp; English.
                                                                                                                                                                                                administering recombinant adeno-associated vectors which express blood
                                                                                                                                                                                                     coagulation factor VIII
                                                                                                                                                                                                           Treating blood clotting disorder, especially hemophilia in mammals,
                                                                                                                                                                                                                                                           WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                                         Couto LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Adeno associated virus.
Chimeric - Mus sp.
Chimeric - Homo sapiens.
Chimeric - Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                  (AVIG-) AVIGEN INC.
                                                                                                                                                                                                                                                                                                                                               22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200145510-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11900 tgccttagtatttccttcaagctgcccctgcagg 11933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11840 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 11899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAV-F8-1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11780 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 11839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD08612 standard; DNA; 11933 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11720 tgaatageegaegeetttgeatetteegeaetetttetegaeaaeteteeeeeaeagete 11779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11660 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 11719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lood_clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 tgccttagtatttccttcaagctgcccctgcagg 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                     Colosi PC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 backbone. It comprises HNF-3 mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EFlalpha) and immunoglobulin G based on human elongation factor lalpha (EFlalpha) and immunoglobulin G (196) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV sequence poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the light and heavy chains of human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11240 tetteaegattategaeteaatgetettaeetgttgtgeagatataaaaaateeegaaae 11299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11180 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 11239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11933 BP; 3258 Å; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11360 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 11419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11420 gtagtaagegeegeetetttteateteactaceacaaegagegaattaaeceategttga 11479
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11480 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
                                                                                                                                                                                                                                                                                                11600 tttgtggcattgcaccaccagagtgtcatacagcggcttaacagtgcgtgaccaggtggg 11659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ttccggtattcgcttaattcagcacaacggäaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 tcttcacgattatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 aaaggeegeagegtaactattactaatgaatteaggacagacagtggetacggetcagtt 120
                                                                                                                                                 11720 tgaatagoogacgcotttgcatcttccgcactctttctcgacaactctcccccacagctc 11779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
11840
                                                                     11780 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 gtagtaagcgccgcctcttttcatctcactaccacaacgagcgaattaaccccatcgttga 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                           661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                             541 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc
                841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 11359
                                                                                                                                                                                                                                                                                                                                                                            gtggcaatcatgctgctaacgtgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 11599
                                                                                                                                                                 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                         ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 11719
                                                                                                                                                                                                                                                                                                                     tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                          tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 840
cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 11899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 934; DB 22; 100.0%; Pred. No. 4.9e-312; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 11933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT
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XXTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA11992 standard; DNA; 37856 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA11992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant-protection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3398..6100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (8433..9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (6374..7111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*rtag= a
/product= "ORF1-tRNA synthetase"
                                                                                                                                                                                                                                                 9855..11393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "gtg start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "ORF2-monooxygenase"
                                                                                                                                                                                                                                                                                           /product= "ORF6-polyketide synthase"
20003..27889
                                                                                                                                                                                                                                                                                                                             /note= "ACC start codon"
15374 ..19984
                                                                                                                                                                                                                                                                                                                                                  /product= "ORF5-3-oxoacyl-ACP-reductase
                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF4- tyrosine/DOPA-Decarboxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                           note= "AGT start codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "ORF3-aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                 /note= "GTG start codon"
                                                                                                                                                                                                                               /product= "ORF8-transpeptidase" complement (30040..31720)
                                                                                                                                                                                                                                                                                                                                                                        12212..13658
                                                                                                                                                   /product= "ORF10-transcription regulator" 33128..33613
                                                                                                                                                                                     31982..32932
                                                                                                                                                                                                       /product= "ORF9-regulation element"
                                          /product= "ORF13-transcription regulator" complement (35730..36242)
                                                                                     /product= "ORF12-regulation element"
                                                                                                              33661..34077
                                                                                                                      /product= "ORF11-regulation element"
/note= "GTG start codon"
                                                                          complement (35255..35616)
           /product= "ORF14-transcription regulator"
/note= "GTG start codon"
                                                                                                                                                                                                  "CGC stop codon"
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DE19846493-A1.

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RESULT
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05-MAR-1999;
09-MAR-1999;
                                                                25-FEB-2000; 2000EP; 0301439.
                                                                                        06-SEP-2000.
                                                                                                             EP1033405-A2
                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                25127 gggcatctcgcgctggagctcgagcagccgcggccctacggcgatta 25173
                                                                                                                                                                                                                                                                                                                                       25067 tcgacacaaatcttgctcaaagaagtgttcacgctctacgaggcgcaccgcgggacaccgt 25126
                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 17282.
                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                                                                        AAC37411;
                                                                                                                                                                                                                                                    AAC37411 standard; DNA; 1063 BP.
                                                                                                                                                                                                                                                                                                            816 ggcaatctctgcatcttgcccccggcgtcgcggcactacggcaataa 862
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37856 BP; 5655 A; 13666 C; 12913 G; 5622 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and/or immunosuppressant and antibiotic and antifungal activities and are useful as plant-protection agents. This sequence represents the DA sequence represents the DA mathematical from Sorangium cellulosum which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products effect or are involved in the enzymatic biosynthesis, compounds (II). (I) can be inserted into an expression vector and used to transform or transfect prokaryotic or eukaryotic cells with the aim of obtaining strains that produce large amounts of polyketide or heteropolyketide compounds, especially epothilones, which have cytotoxic
                                                                                                                                                                                                                                                                                                                                                          756 tetegacaaeteteeceeaaagetetgttttggcaatateaacegcaeggeetgtaecat 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel DNA sequence (I) whose expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 20-33; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beyer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mueller R;
            99US-0123180、
99US-0123548
99US-0125788
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                              99US-0121825
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                                                                                                                                                                                                                                                                                                                                                                                                 3.98;
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                               Score 36.6; DB 21; Length 37856; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
                            13-JUL-1999;
                                                                                                                                                                                 18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
                                       12-JUL-1999;
                                                                     06-JUL-1999;
                                                                                                                                                               22-JUN-1999;
23-JUN-1999;
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18 - MAY - 1999
19 - MAY - 1999
20 - MAY - 1999
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07-MAY-1999
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                                                                                                         99US-0140823.
99US-0140991.
99US-0141287.
               99US-0143542
99US-0143624
                                                                                                                                                                                99US-0139463.
99US-0139750.
99US-0139763.
99US-0139817.
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99US-0139460
99US-0139461
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99US-0142055
                                                      9908-0142803
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99US-0140354.
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99US-0137502.
99US-0137724.
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99US-0139454
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99US-0138540
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990S-0134219
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990S-0134370
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990S-0134941
990S-0135124
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99US-0134256.
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99US-0132486.
99US-0132487.
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99US-0136021
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99US-0126785
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16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

99US-0144086.
99US-0144331.
99US-0144332.
99US-0144334.
99US-0144334.
99US-0144335.
99US-0144335.
99US-0144336.
99US-0144863.
99US-0144864.
99US-0145086.
99US-0145086.
99US-0145087.
99US-0145087.
99US-0145087.
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99US-0145087.

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RESULT 5
AAF28541
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Best Local S
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12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
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14-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                              AAF28541 standard; DNA; 49617 BP
                                                                                                                                                                                                                                                    466 ttaacccatcgttgagtcaaatttacccaattttattcaataagtcaatatcatgccgtt 525
                                                                                                                                              04-APR-2001 (first entry)
                                                                                                                                                               AAF28541;
                                                                                                                                                                                                                     986 tgcctttatgtcttcat 1002
                                                                                                     Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                            Genomic fragment #28.
                                                                                                                                                                                                                               586 tgcgattgactcttctt 602
                                                                                      Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                        WO200078968-A2
       (INCY-) INCYTE GENOMICS INC
                       18-JUN-1999; 99US-0140121
                                       16-JUN-2000; 2000WO-US16649
                                                       28-DEC-2000
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0158232

99US-0158369

99US-0159294

99US-0159295

99US-0159330

99US-0159330

99US-0159637

99US-0159637

99US-0159684

99US-0160741

99US-0160768

99US-0160776

99US-0160776

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99US-0160776
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99US-0160981.
99US-0160989.
99US-0161404.
99US-0161405.
99US-0161406.
99US-0161350.
99US-0161361.
                                                                                                                                                                                                                                                                                                                                                         99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                 3.5%;
                                                                                                                                                                                                                                                                                                                          Score 33; DB 21; Length 1063; Pred. No. 0.88; O; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                  0;
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99US-0145224 99US-0145276 99US-0145918 99US-0145919 99US-0145951 99US-0146386 99US-0146388 99US-0146389 99US-0147038 99US-0147204 99US-0147204 99US-0147204 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147303 99US-0147416 99US-0147935

20-JUL-1999;
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23-JUL-1999;
23-JUL-1999;
23-JUL-1999;
24-AUG-1999;
27-JUL-1999;
28-AUG-1999;
29-AUG-1999;
30-AUG-1999;
30-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AU

990S-0148341 990S-0148341 990S-0148565 990S-0149368 990S-014975 990S-0149722 990S-0149722 990S-0149723 990S-0149929 990S-0149929 990S-0149929 990S-0149929 990S-0149929 990S-0149930 990S-0150566 990S-0150568

99US-0191066

990S-0151080 990S-0151308 990S-0151438 990S-0152363 990S-0153070 990S-0154018 990S-0154018 990S-0154039 990S-0155139 990S-0155486 990S-0156458 990S-0156458 990S-0156458 990S-0157513

99US-0158029÷

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RESULT 6
AAI12818/c
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                                                                                           04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         11682 cggatgag 11689
                                                        21-SEP-2000;
                                                                    03-AUG-2000;
                                                                                                                         30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11562 cacagettgatgatgticaaagettggataategteetgetgaagaaacaccaegeteat 11621
                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                               WO200157278-A2
                                                                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                  Probe #2751 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                        11622 tgggtcgtatgacagtgactttaggcgctacttctgcaccacaagcggctgatacaacaa 11681
                                                                                                                                                                                                                                                                                        12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                          AAI12818 standard; DNA; 469 BP
                                                                                                                                                                                                                                                                                                                         AAI12818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention the titles to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large composition of the catarrhalis (Branhamella catarrhalis) is a large flora of human upper airways. M. catarrhalis is known to cause acute, infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                   637 cttaacag 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 aatgitgictgogattgactcttotttgiggcattgcaccaccagagogicatacagogg 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 catgccgttaatatgttgccqtccgtggcaatcatgctgctaacgtgtgaccgcattcaa 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49617 BP; 14572 A; 9853 C; 11026 G; 14166 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 235-247; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-041427/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                      2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
                        2000GB-0024263.
                                                                                         2000US-0207456.
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53.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 22; Length 49617; Pred. No. 16;
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AAI34173/c
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0236687.

27-SEP-2000; 2000US-0235359.
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                     WPI; 2001-488897/53.
                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                 Penn SG, Hanzel DK,
                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                      WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                 Probe #2859 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI34173 standard; DNA; 469 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 cgcatttggtgatccggttctgcttccggta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CAGACAGAAGCAGAGATTGAGTGGGGGGGGTGCTGTGGTTGCTTGGAGGACAAGTGGCAAGTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 2751; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 cagacagtygctacggctcagtttgggttgtgctggttgctgggcggcgatgacgcctgta 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53.
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                                                                                                                                       2000GB-0024263.
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                                                                           Chen W, Rank DR;
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Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 469;
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SXCCCCCXXX
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AAI02735/c
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   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 469 BP; 125 A; 159 C; 88 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI02735 standard; DNA; 469 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast cancer; development disorder; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #2726 used to measure gene expression in human breast sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease; proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157270-A2
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases, with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 cagacagtggctacggctcagtttgggttgtgctgttgctgggcggcgatgacgcctgta 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 25
                                                                                                                                                Claim 25; SEQ ID No 2726; 322pp; English
                                                                                                                                                                                            Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                             WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgcatttggtgatccggttctgcttccggta 188
                                                                                                                                                                                a human breast
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                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0180312.;
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry) .
                                                                                                                                                                                                                                                                                                                             2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.4%;
59.3%;
                                                                                                                                                                                                                                                                 Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 469 BP; 125 A; 159 C; 88 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI18836 standard; DNA; 542 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI18836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #8769 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 cgcatttggtgatccggttctgcttccggta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 CAGACAGAAGCAGAGATTGAGTGGGGGGGGGTGCTGGGTTGCTTGGAGGACAAGTGGCAAGTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
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                        from human HeLa cells. The SENPS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a magne derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging expression, the cervix, notably cervical cancer. Of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                            analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 25
                                                                                                                                                 The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                Claim 25; SEQ ID No 8769; 487pp; English.
                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
           at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                    The present sequence is one such probe. The SENPs are derived man HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359
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AAI43958/c
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                                                                                                               Sequence 542 BP; 150 A; 153 C; 121 G; 118 T; 0 other;
                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                     Human genome-derived \sin \dot{\hat{q}} exon nucleic acid probes useful for analyzing gene expression in human placenta -
278 CAGACAGAAGCAGAGATTGAGŢĠGGGGTGCTGTGGTTGCTTGGAGGACAAGTGGCAAGTC 219
                                                                                                                                                                                                                  Claim 25; SEQ ID No 12644; 654pp; English.
                                                                                                                                                                                                                                                                                    WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
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27-SEP-2000;
               98 cagacagtggctacggctcagtttgggttgtgctgttgctggtgggcggcgatgacgcctgta 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #12644 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 CAGACAGAAGCAGAGATTGANTGGGGGGTGCTGGTTGCTTGGAGGACAAGTGGCAAGTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 cagacagtggctacggctcagtttggggttgtggtggtgggcggtgacgcctgta 157
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                                                                       Similarity
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                                                           Conservative
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2000US-0632366
2000US-0234687
2000US-0236359
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                                                                    3.4%;
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59.3°;
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Pred. No. 1
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Pred. No. 1.6;
                                                                           DB 22; Length 542;
                                                    37; Indels
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AAF58252/c
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489 tacccaattttattcaataagtcaatatcatgccgttaatatgttgccatccgtggcaat 548
                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other:
                                            434 ИМИИИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИТААGCИМИМИМИМИМИМИМИМИМ
                                                                                                   369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
                                                                                                                                                              309 aggctctaactattacctgcgaactgtttcgggattgcattttgcagacctctctgcctg 368
                                                                                                                                                                                                                         249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-159728/16
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                                                                                                                                                                                                                                                                                              Local Similarity 1.7%;
nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 188
                                                                     C9CC9CCtCttttcatctcactaccacaacgagcgaattaacccatcgttgagtcaaatt 488
                                                                                                                                                                                                                                                                                     Conservative 196; Mismatches 153; Indels
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                                                                                                                                                                                                                                                                                                      3.4%; Score 31.8;
1.7%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                 DB 22; Length 936;
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                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-159728/16.
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                                                                                                                                                                                                                                                                                                                       a single surface
                                                                                                                                                                                                          Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                               monitoring gene expression.
                                                                                                                   249 attatogactcaatgotottacotgttgtgcagatataaaaaatcccgaaaccgttatgc 308
434 ЖИМЖИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИТААССИМИМИМИМИМИМИМИМИМ
                                      369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
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                  cgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttgagtcaaatt 488
                                                                             Similarity
                                                                                                                                                              Conservative 196;
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                                                                                                                                                                       3.4%; Score 31.8;
1.7%; Pred. No. 2.1;
                                                                                                                                                                                  Score 31.8;
                                                                                                                                                                Mismatches 153;
                                                                                                                                                                                   DB 22; Length 936;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2000; 2000WO-US20476.
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17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monitoring gene expression.
                                                                                                                                                                                                                               309 aggctctaactattacctgcgaactgtttcgggattgcatttttgcagacctctctgcctg 368
                                                                                                                                                                                                                                                                       249 attatcgactcaatgctcttacctgttgtgcagatataaaaaaatcccgaaaccgttatgc 308
           429 cgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttgagtcaaatt 488
                                                          369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
                                                                                                                                                                                                                                                                                                                                   Match 3.4%;
Local Similarity 1.7%;
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Score 31.8;
Pred. No. 2.1;
    DB 22; Length 936;
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RESULT 14
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Sequence 936 BP; 6 A; 138 G; 8 G; 8 T; 776 other;
                      369 cgatggttggagttccagacgatacgtogaagtgaccaactaggcggaatcggtagtaag 428
                                                 monitoring gene expression.
                                                                                                                         249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
                                                                                                                                                                                                                                                                                                                                     Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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17-MAR-2000; 2000US-6190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression; ss
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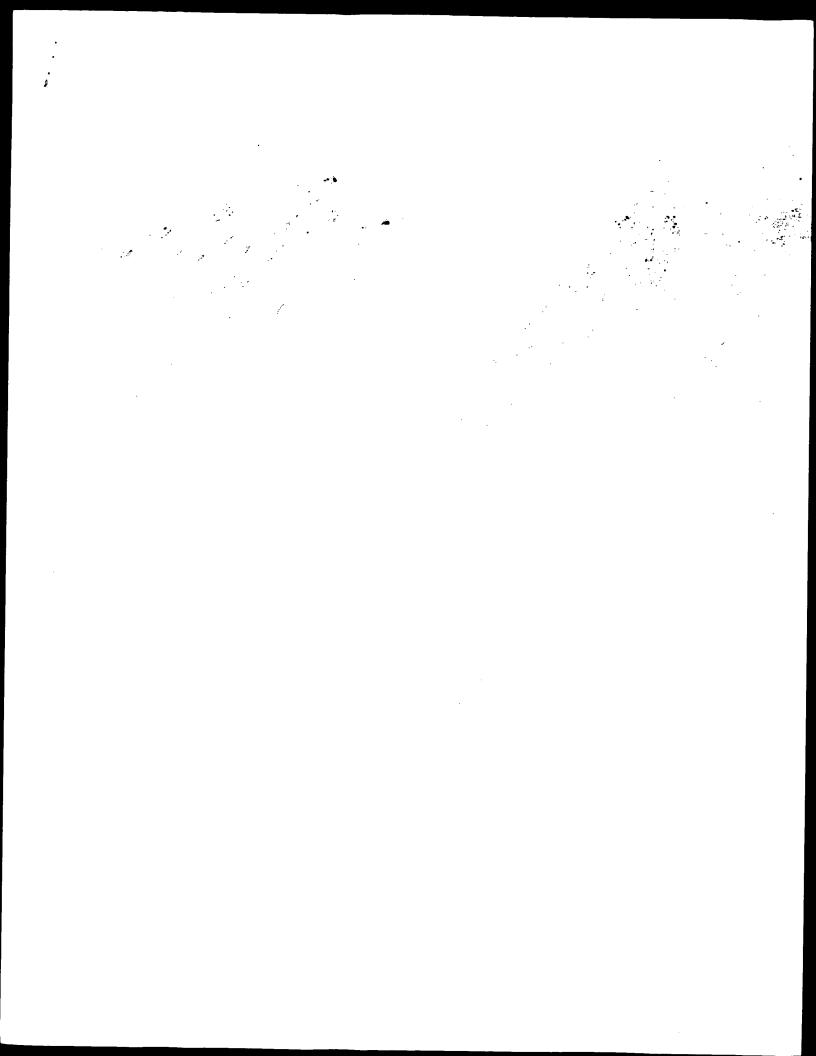
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309 aggototaactattacotgogaactgtttcgggattgcattttgcagacototctgcotg 368

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                                                                                                                                                                 Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
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                                                                                                    Local Similarity
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gene expression; ss.
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                                                                        3.4%; Score 31.8; DB 22; Length 9 ilarity 1.7%; Pred. No. 2.1; Conservative 196; Mismatches 153; Indels
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54	489 tacccaattttattcaataagtcaatatcatgccgttaatatgttgccatccgtggcaat 548	489	Qy
3/	434 WWWWWWWWWWWWWWWWWWWWWWWWWWTAAGCWWWWWWWWWW	434	Db
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Search completed: January 8, 2002, 17:29:38 Job time: 12758 sec



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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 200000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/
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## SUMMARIES

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11933 4 7218 1 7	Length DB
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Application US/0 00560 MATION: MATION: OULD, Linda B. OULD, Linda	3.1 1955 2 US-08-47 3.1 1955 3 US-08-48 3.1 1955 4 US-08-89 3.1 1955 4 US-08-89 3.0 7742 2 US-08-89 3.0 4403765 4 US-09-1 3.0 4411529 4 US-09-1 3.0 1142 1 US-08-1 3.0 1142 1 US-08-4 3.0 1142 1 US-08-4 3.0 2696 1 US-08-2 3.0 2696 1 US-08-2 3.0 2696 1 US-08-2 3.0 3068 1 US-08-2 3.0 3068 1 US-08-2 3.0 3068 1 US-08-4 3.0 3068 1 US-08-4 3.0 3068 1 US-08-4
vectors for Exp., 618 )	US-08-478-373-114 US-08-483-577A-114 US-08-483-577A-114 US-08-897-438-114 US-08-882-704A-4 US-08-882-704A-4 US-08-103-840A-2 US-09-103-840A-1 US-08-105-483-87 US-08-105-483-87 US-08-105-483-87 US-08-105-483-87 US-08-101-87 US-08-217-438-1 US-08-217-438-1 US-08-217-438-1 US-08-310-584-1 US-08-310-584-1 US-08-310-584-3 US-08-310-584-3 US-08-310-584-3 US-08-310-584-3 US-08-950-720A-7
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US-09-364-862-13

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CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
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                                                                                                                 SEQ ID NO 13
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: CELLS 1.
FILE REFERENCE: AVIGEN-03743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 11900 tgccttagtatttccttcaagctgcccctgcagg 11933
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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11900 tgccttagtatttccttcaagctgcccctgcagg 11933
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                                                11840 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 11899
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                                                                                                           11780 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 11839
                                                                                                                                                                      11720 tgaatageegaegeetttgeatetteegeaetetttetegaeaaeteteeeeeaeagete 11779
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                901 tgccttagtatttccttcaagctgcccctgcagg 934
                                                                                                                                                                                                                                                                                               11600 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 11659
                                                                                                                                                                                                                                                                                                                                                          11540 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 11599
                                                                 841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                      11480 gtcaaattttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
                                                                                                                          781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11360 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 11419
                                                                                                                                                                                       721 tgaatagocgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                   661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11300 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 11359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11180 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 11239
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                                                                                                                                                                                                                                                                                                                                                                                                                                    481 gtcaaattttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11000 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 11059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 100.0%; Score 934; Local Similarity 100.0%; Pred. No. 0;
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Med Jan 9 14:38:17 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent NO. 5670367
Patent INFORMATION:
GENERAL INFORMATION:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, RECONSINANT FONLPOX VIRUS
APPLICANT: VINENTION: CO
TITLE OF CENTENTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF STREET: 1800 Diagonal Road, STREET: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EV 34 1.4"

APPLICATION NUMBER: 1991

APPLICATION 126-AUG-1991

EILING DATE: 1XFORMATION:

EILING DATE: 1XFORMATION:

ATTORNEY/AGRIT STEPHER: 3,768

ATTORNEY/AGRIT STEPHER: 30472

NAME: BENT NUMBER: 30472

NAME: SEPENCE/DOCKET INFORMATION:

REFERENCE/DOCKET INFORMATION:

REFERENCE/DOCKET INFORMATION:

TELECOMMUNICATION 3083-4109

TELECHARACTERISTICS:

INFORMATION FOR TERISTICS:

INFORMATION FOR TERISTICS:

INFORMATION FOR TERISTICS:

SEQUENCE 77218 bacid

TYPE: CHARACTERISTICS:

STRANDEDNESS: Single

TYPE: STRANDEDNESS: SINGLE

TYPE: STRANDEDNESS: SINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSITICATION: 435
CLASSITICATION DATA:
CLASSITION NUMBER:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: pTZ9pt-F1s
CLONE: 1463-14
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4.0%; Score 37.6; DB 1; Indels
Ouery Match
Best Local 5; Conservative 152; Mismatches
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       730 gargoottegcateteccocatetetetectcgacaactctcccccacagctctgttttggc 789
                                                                                                                                                                                                                                                                                       790 aatatoaacegcacggcetgtaccatggcaatctctgcatcttgcccccggcgtcgcggc
                                                                                                                                           850 actacggcaataatoogcataagcgaatgttgcgagcacttgcagtacctttgccttagt 909
1298 אייאיאיאיאיאיאיאיאיאיא 1317
                                                                     910 attroctromagorgococt 929
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Patent INFORMATION:

APPLICANT: Fett, Karen A.

APPLICANT: Olson, Antisense Inhibition of Angiogenin Expression

FILE OF REPERIOR: 10498/05286

FILE OF SEPLICANTON NUMBER: 60/041182

CURRENT APPLICANTON NUMBER: 60/041182

CURRENT FILING DATE: 1997-03-21

EARLIER FILING DATE: 1997-03-21

EARLIER FILING DATE: 1997-03-21

SOFTMARE: Patentin Ver. 2.0
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NAME/KEY: CDS (1809)..(2252)

LOCATION: (1809)...

109-045-301-1
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RESULT 195-868-11/C LOTION US/09195868

Sequence 11 00080AT NOW MICHAEL

RESULT NO. CORMANDOM MD, MICHAEL

RESULT NO. MICHAEL

RESULT NO. MICHAEL

RESULT NO. MICHAEL

RESULT NO. STREET

RESULT NO. STREET

RESULT NO. STREET

RESULT NO. STREET

RESULT NO. MICHAEL

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3.4%; Score 31.6; DB 4; Length 4¢
9.2%; Pred. No. 1.4; 59; Indels
9.2%; Pred. No. 1.4; 59; Indels
9.53.2%; O; Mismatches
9.54 Local Similarity 53.2%; O; Mismatches
9.55 Local Conservative
9.56 Local Conservative
9.57 Local Conservative
9.57 Local Conservative
9.58 Local Conservative

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CORRECT PARAMETER FORM: 115k

CMEDITER READ.

COMPUTER: BM PC COMPOSIMS DOS VETSION #1.30

COMPUTER: PC DOS/MS DO, VETSION #1.30

COMPUTER: PARAMETER PARAMETER
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                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: US/09/195,868
APPLICATION NUMBER: US/09/195,868
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B: CHIRON STREET

4560 HORTON STREET
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1182.004

ATELIANG LANTE:
NAME: NEGROUS AGENT INFORMATION:
REGISTRATION LEIGH H.
REFERENCE\_POCKETHER: 36.831
TELECOMMUNICATION INFORMARE: 1182.
FELEPHONE: 510-652-32707
SEGUENCE\_FOR SEQ 13 54.2
LENGTH: 3691 BASTETICS: 12:
TYPE: 3691 BASTETICS: 12:
TYPE: 13691 BASTETICS: 12:
TYPE: 1000 BA

1182.004

COMPUTER TOWN
MEDIUM TYPE:
COMPUTER: FORM:
COMPUTER: IBM PC
SOFTWARE: IBM PC
COMPOTER: IBM

Release #1.0, Version #1.30

94608 RE-

CLASSIFICATION:
APPLICATION:
FILING DATE: US/09/195,868

APPLICANT CHMATION:
APPLICANT KAVANAUGH MD, MICHAEL
PRICANT: POT PH.D., DAVID
TITLE OF INVELTIANS MOPHD, LEWIS T.
CORRESPONDENCES: 5-PHOSPHATASES (SIPS)
STREET: EMERYTON SICHAPASES (SIPS)
STREET: EMERYTON STREET:
CATTY: EMERYTON STREET
STATE: CANTILLE

APPLICANT: ASO HORDON CORPORATION
STATE: CANTILLE

APPLICANT: ASO HORDON STREET
CANTILLE

APPLICANT: CANTILLE

APPLICANT: ASO HORDON STREET
COLUMN
C

INOSITOL POLYPHOSPHATE

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609 attgcacc 616 || || || || 1 1581 ATAGCACC 1574

Ouery Match
Best Local Similarity 3.38; Score 31.2;
Matches 45; Conservative 0; Mismatches

GENERAL

2, Application US/09195868

.09-195-868-12/c tent No.

US-09-195-868-12

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1588 ATAGCACC 1581

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US-09-418-540-1/c
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APPLICANT: Pot, D
                                                                                                                                                                                                                                                                                                                       Query Match 3.3%; Score 31.2; DB 4; Length 4147; Best Local Similarity 66.2%; Pred. No. 1.9;
              Sequence 7, Application US/08664962B Patent No. 6218162 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
APPLICANT: NUENTION: NO. 6296848el Grb2 Associating Protein and Nucleic TITLE OF INVENTION: Acids Encoding Therefor NUMBER OF SEQUENCES: 10 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,540
FILING DATE: 14-OCT 1999
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APPLICATION NUMBER: U6:08/560,005
FILING DATE: 17-NOV-1545
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SEQUENCE CHARACTERISTICS:
LENGTH: 4147 base pairs
TYPE: nucleic acid 
TYPE: nucleic acid 
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              1648 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) .
                                                                                                                                                    1588 ATAGCACC 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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APPLICANT: Krystal, Gerald
                                                                                                                                                                                                                                                               549 catgctqctaacqtqtgaccgcattcaaaatgttqtctgcqattgactcttctttqtggc 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dow, Karen B. 29,684
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                         609 attgcacc 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                             45; Conservative
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17..2944
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                                                                                                                                                                                                                                                                                                                 0; Mismatches
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US-08-664-962B-7
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                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                        Sequence 7, Application US/09311743
Patent No. 6238903
GENERAL INFORMATION:
APPLICANT: KTYSTA1, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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LENGTH: 4870 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       2377 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 2318
                                                                                                                                                                                                                                                                                                                           2317 ATAGCACC 2310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mueller, Douglas P. REGISTRATION NUMBER: 30,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 14-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         609 attgcacc 616
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TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 66.2%; les 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSHIP
                                                                             STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
                                                                                                                                ADDRESSEE:
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                 BERESKIN & PARR
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pred. No. 2;
0; Mismatches 23; Indels 0;
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US-09-007-005-17

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US-09-007-005-17/c
Sequence 17, Application US/09007005B
Patent No. 6258558
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                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17
                                                                                                                                                                                                                                                                        APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
FABSITED ADDITION NUMBER: 60/715 063
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
OTHER INFORMATION: n = A,T,C or G
                 NAME/KEY: misc_feature LOCATION: (1)...(289)
                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                                             OTHER INFORMATION: Translation template
                                                           FEATURE:
                                                                                                                                                  ENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2377 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 2318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/311,743
FILING DATE: 14'-May-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GTavelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7771-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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Pred. No. 2;
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: NAME/KEY: misc_feature
: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/05,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
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Best Local Similarity 5.7%; Pred. No. 0.45;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Szostak, Jack W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
127 YNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 68
                                            825 tycatcttycccccggcytcgcggcactacggcaataatccgcataagcgaatgttgcga 884
                                                                                                187 YNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 128
                                                                                                                                            765 ctctcccccacagctctgttttggcaatatcaaccgcacggcctgtaccatggcaatctc 824
                                                                                                                                                                                                247 YGYAYGYTYTYAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 188
                                                                                                                                                                                                                                          705 egettgetggeateettgaatageegaegeetttgeatetteegeaetetttetegaeaa 764
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                                                                                                                                                                                                                                                                                                 13; Conservative 95; Mismatches 119; Indels
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3; Pred. No. 0.45;
95; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                Matches
                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                      REGISTRALLON NOTIFICATION 1038
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                              FEATURE:
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                             837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
                                                                                 777 getetgittiggeaatateaacegeacggeetgtaceatggeaatetetgeatettgeee 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08 FILING DATE: 08-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
925 CTAGTTCTTCAGCATTAGGCCCCATAAAAACCACCTTCTAATGTTCC 880
                                                            APPLICATION NUMBER: US/08/487,890A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                                           Match 3.3%;
Local Similarity 55.7%;
les 59; Conservative
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                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                           nucleic acid
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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                                                                                                                               y; Score 30.8; DB
y; Pred. No. 1.6;
0; Mismatches
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0;

Gaps

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RESULT 14
US-08-478-435-112/c
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                                                                                                                   Matches
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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925 CTAGTTCTTCAGCATTAGGCCCATAAAAACCACCTTCTAATGTTCC 880
                          837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
                                                                        777 getetgttttggcaatateaacegeacggeetgtaceatggcaatetetgcatettgeec 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08 CLASSIFICATION:
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                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael REGISTRATION NUMBER: 2
                                                                                                                              y Match 3.3%; Score 30.8; DB 2; Length 1951; Local Similarity 55.7%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                               LENGTH:
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Klein, Michel
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Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                  1951 base pairs
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                                                                                                                    Conservative
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08-NOV-1994
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                                                                                                                      0; Mismatches
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                                                                                                                            47; Indels
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Search completed: January 8, 2002, 17:21:33 Job time: 12344 sec
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; LOCATION: 1..1890
US-08-337-483-112
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NAME: Stewart, Mighael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEPAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
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US-08-337-483-112/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 30.8; DB 2; Length 1951; Best Local Similarity 55.7%; Pred. No. 1.6; Matches 59; Conservative 0; Mismatches 47; Indels 0;
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APPLI
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOW-1994
CLASSIFICATION: 465
CLASSIFICATION: 465
                                                                                                                                                                            925 CTAGTTCTTCAGCATTAGGCCCATAAAAACCACCTTCTAATGTTCC 880
                                                                                                                                                                                                                             837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite CITY: Toronto STATE: Ontario
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COUNTRY: Canada
ZIP: M5G 1R7
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Schryvers, Anthony
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Copyright (c) 1993; 2000 Compugen Ltd.
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## SUMMARIES

	O	C	o :	Result
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419.4 387.2 380.2	455.4 454.2 420.6	569.6 531.4	724.4	Score
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## ALIGNMENTS

source	FEATURES	REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AV404408 LOCUS DEFINITION
	Genome Research Group National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nirs.go.jp method:uni-directional, sequence direction:sequenced from T3 primer (5' -> 3') Project='Silkworm Genome Program in MAFF, and Research for the Project='Silkworm Genome Program in MAFF, on the Future Program in JSPS'. see 'SilkBase', Chttp://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb. Location/Qualifiers	<pre>pukaryota; Metazoa; Arthropoda; Trached A. Hearyota; Metazoa; Arthropoda; Prerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia percygota; Neoptera; Endoptera; Endoptera; Combyx.  1   (bases 1 to 734) 1   (bases 1 to 734) Mita, K., Morinyo, M., Shimada, T., Okano, K. and Maeda, S. Bombyx mori CDNA Bombyx mori CDNA Unpublished (2000) Contact: Mita K Contact: Mita K</pre>	AV404408 AV404408.1 GI:6908496 EST. domestic silkworm. Bombyx mori	AV404408 734 bp mRNA EST 06-FEB-2000 AV404408 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg0946 T3, mRNA sequence.

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                                    AIO65168 628 bp mRNA EST 24-JUL-1998 ESTTRA-8 Rat Lambda Zap II Library, Stratagene #936501 Rattus norvegicus cDNA clone pGEM-T/TRKA-8ME 3', mRNA sequence.
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/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult
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           148
                 672 ttgggattagcatcgtcacagogcgatatgctgcgcttggctggcatccttgaatagccga
                                                                                612 gcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtgggttgggttagggt
                                                             208 GCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGGTTGGGTAAGGT 149
                                                                                                                            268 GCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTCTTTGTGGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Contact: DongBing Lai
Contact: DongBing Lai
National Laboratory of Medical Molecular Biology
Chinese Academic of Medical Sciences & PUMC
5 Dongdan Santiao, Beijing 100005, P.R.China
Tel: 86-10-65296406
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Seq primer: M13 Forward Primer.
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/dev_stage="6 weeks"
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/db_xref="taxon:10116"
/clone="pGEM-T/TRKA-8MF"
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                                                                                                                                                          149 acgcctgtacgcatttggtgatccggttctgcttccggtattcgcttaattcagcacaac 208
                                                                                                                                                                                                                                89 aattcaggacagacagtggctacggctcagtttgggttgtgctgttgctgggcggcgatg 148
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                                                                                                                                                                                                             acctgttgtgcagatataaaaaatccccgaaaccgttatgcaggctctaactattacctgc 328
                                                                   GGAAAGAGCACTGGCTAACCAGGCTCGCCGACTCTTCACGATTATCGACTCAATGCTCTT 181
                                                                                    ggaaagagcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctctt 268
                                                                                                                                         ACGCCTGTACGCATTTGGTGATCCGGTTCTGCTTCCGGTATTCGCTTAATTCAGCACAAC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.: Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Samuel Roberts Noble Foundation The Samuel Roberts Noble Foundation OK 73402, USA
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: 092 row: G
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                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Drought"
/tissue_type="plantlets"
/tissue_type="poled timepoints"
/dev_stage="pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entiplantlets harvested in a series of days post watering plantlets harvested in a series of days post watering
                                                                                                                                                                                                                                                                                                                                                                                                             timepoints.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 CTACCACAACGAGCGAATTAACCCATCGTTGAGTCAAATTTACCCCAATTTTATTCAATAA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 ctaccacaacgagcgaattaacccatcgttgagtcaaatttacccaattttattcaataa 508
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AI489217
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Email: http://www.genome.clemson.edu/orders/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
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                                                                                 166
                                                                                                               /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: xho1; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites,
                                                                                              respectively."
                                                                                                                                                                                    /tissue_type="carpel"
/tissue_type="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF/"
                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="cLED17L7"
                                                                                                                                                                                                                                                                                                             organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                          /clone_lib="tomato ovary, TAMU"
                                                                                                                                                                                                                                                                                            /cultivar="TA496"
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Score 569.6; DB 10 Pred. No. 1.1e-163;
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                      DB 10;
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Query Match

Best Local Similarity

61.0%;

Matches

572;

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AUTHORS
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                                                                                                                    Clemson University
                                                                                                                                 Clemson University Genomics Institute
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                                                                 mail: http://www.genome.clemson.edu/orders/index.html
prime sequence.*
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                                                                                                  Jordan Hall, Clemson,
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/cultivar="TA496"
                                                 Location Qualifiers
          /organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 CAATCATGCTGCTAACGGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTCTTT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCGGTAG
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   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                         Bombyx mori
                                                                                                                                                    domestic silkworm.
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                                                                                                                                                                                                               AV404019.1 GI:6908107
                                                                                                                                                                                                                                                       AV404019 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg--0345 T3, mRNA sequence.
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(bases 1 to 714)
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/dev_stage="3-8mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="vector: pBlueScript Sk(-); Site_1: EcoR1; Site_2: EcoR1; Site_2: EcoR1; Site_2: EcoR1; Site_2: EcoR1; Site_2: Ec
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                                                                                                                                                                                                                                                                                                                                            714 bp
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Pred. No. 5.4e-152;
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Best Local
LOCUS BE420137 743 bp mRNA EST 24-JUL-2000 DEFINITION WWS020.E9R000101 ITEC WWS Wheat Scutellum Library Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 tgaccaactaggcgggaatcggtagtaagcgccgctcttttcatctcactaccaccaacga 460
                                                                                                                                                                                                                                                                                                                                                                                                                                          461 gcgaattaacccatcgttgagtcaaatttacccaattttattcaataagtcaatatcatg 520
                                                                                                                                                                                                                                                                                                                                                                                  181 TTGTCTGCGATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCGAATTAACCCATCGTTGAGTCAAATTTACCCCAATTTTATTCAATAAGTCAATATCATG 120
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Local Similarity 99.2%;
                                                                                                                                                    1 TGACCAACTAGGCGGAATCGGTAGTNAGCGCCGCCTCTTTTCATCTCACCTACCACAACGA 60
                                                                                                                                                                                                                                                                                                                                            acagtgcgtgaccaggtgggttgggtaaggtttgggattagcatcgtcacagcgcgatat 700
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                                                                                                                                                                                                             ACAACTCTCCCCCACAGCTCTGTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAA 420
                                                                                                                                                                                                                              acaactetececeacagetetgttttggcaatatcaacegcaeggcetgtaceatggcaa 820
                                                                                                                                                                                                                                                                                                                           ACAGTGCGTGACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Future Program in JSPS'. see 'SilkBase', for whole ESTdb <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institute of Radiological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project='Silkworm.Genome Program in MAFF, and Research for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kmita@nirs.go.jp
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/strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"
/dev_stage="newly-eclosed adult"
/ 200 c 158 g 195 t
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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0; Mismatches
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                                                                                                                                                                                                                                                                      577
757 ctcgacaactetcccccacagctctgttttggcaatatcaaccgcacggcctgtaccatg
                                                                                                                                                                         637 cttaacagtgcgtgaccaggtgggtttgggtaaggtttgggattagcatcgtcacagcgcg
                                                                         301 ATATECTECCCTTECCATCCTTGAATAGCCGACGCCTTTCCATCTTCCGCACTCTTT 360
                                                                                                                                                     241 CTTAACAGTGCGTGACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaagtgaccaactaggcggaatcggtagtaagcgccgcctcttttcatctcactaccaca 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA clone WWS020.E9, mRNA sequence. BE420137
                                                                                                                                                                                                                               AATGTTGTCTGCGATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAGCG
                                                                                                                                                                                                                                                     aatgttgtctgcgattgactcttctttgtggcattgcaccaccagagcgtcatacagcgg 636
                                                                                                                                                                                                                                                                                                                           catgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattcaa 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifiou, M., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE420137.1 GI:9417983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bread wheat
                                                                                              atatgctgcgcttgctggcatccttgaatagccgacgcctttgcatcttccgcactcttt 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeneca Wheat Improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Schuch W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="scutellum callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ITEC WWS Wheat Scutellum Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="WWS020.E9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum.
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 455.4; DB 10; Length 743; pred. No. 1.3e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 g
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
770 ccccacagctctgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcat 829
                                                      241 GCTGGCATCCTTGAATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTC 300
                                                                         710 gctggcatccttgaatagccgacgcctttgcatcttccgcactctttctcgacaactctc 769
                                                                                                                           181 GACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATATGCTGCGCTT 240
                                                                                                                                              650 gaccaggtgggttgggtaaggtttgggattagcatcgtcacagcgcggatatgctgcgctt 709
                                                                                                                                                                                                                 590 attgactettetttgtgggättgcaccaccagagcgtcatacagcggettaacagtgcgt 649
                                                                                                                                                                                                                                                                121 ATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCCTTAACAGTGCGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                Jocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GCAATCTCTGCATCTTGCCCCCGGCGTCGCGGCACGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          817 gcaatctctgcatcttgcccccggcgtcgcgggcacta 853
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bombyx mori cDNA
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV403989 500 bp mkNa aV403989 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg--0306 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombycoidea; Bombycidae; Bombyx (bases 1 to 500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 a
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult" /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="newly-eclosed adult" 141 c 107 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pheromone gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone="pg--0306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%; Score 454.2; DB 10
99.3%; Pred. No. 2.5e-128;

 Mismatches

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502 AAACGGCAGGAGGTTGTTAGCGCGACCTCCTGCCACCGGCTTTCACGAAGGTCATGTGTA 443

1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60

Matches 456;

Conservative

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Mismatches

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Local Similarity

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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 CTTGCCCCCGGCGTCGCGCCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bb/scripts/gethtml2.pl?tl=QV3&t2=QV3-BN0149-160800-292-905&t3=2000-08-16&t4=1) Seq primer: puc 18 forward ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 47 High quality sequence stop: 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., verjovsxi name, vergovski name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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1 (bases 1 to 617)
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QV3-BN0149-160800-292-g05 BN0149 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                        /note="organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of
                                                                                                                                                                                                           tissue mRNA and cDNA amplification were performed under low stringency conditions."
152 c 151 g 156 t
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/db_xref="taxon:9606"
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45.0%; Score 420.6; DB 11; 98.5%; Pred. No. 5.6e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacct 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NF074F11DT1F1094 Drought Medicago truncatula cDNA clone NF074F11DT 5', mRNA sequence.
                                                                                                                                                                                                                                            Email: gdmay@noble.org
Insert Length: 685 St
Plate: 074 row: F col
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The Samuel Roberts Noble Foundation
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                      163
                      മ
                      timepoints.
                                                   plantlets harvested in a series
                                                                      /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                        /clone_lib="Drought"
                                                                                                                                                              /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                            /clone="NF074F11DT"
                                                                                                                                                           /db_xref="taxon:3
                                                                                                                                                                                                                                                                  Std Error: 0.00
                      169 g
                                                            of days-post-watering
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Best Local Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 TTCCGGTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAGGCTCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcattttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tottcacgattatcgactcaatgctcttacctgttgtgcagatataaaaaaatccccgaaac 300
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                                                                                                                                                                                                                                                                                            Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF003A05IR1F1036 Irradiated Medicago truncatula cDNA clone NF003A05IR 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI269141
                                                                                                                                                               The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
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                                                                                                                                                                                                                                                            Contact: May GD
                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                           Medicago.
                                                                                     Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                         Email: gdmay@noble.org
Insert Length: 688 Std Error
Plate: 003 row: A column: 05
                                                                                                                                                                                                                                      Plant Biology Division
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               /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                       1. .688
/clone="NF003A05IR"
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                                                                                                                               Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAAAATGTTGTCTGCGATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcgatatgc-tgcgcttgctggcatccttgaatagccgacgcctttgcatcttccgcact 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCTTAACAGTGCGTGACCÄGGTĠGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGC
                                             Mita,K., Morimyo,M., Shimada;T., Okano,K. and Maeda, Bombyx mori cDNA Unpublished (2000)
                               Contact: Mita K
                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                   AV404200 775 bp mRNA EST 06-FEB-2000
AV404200 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed
adult Bombyx mori cDNA clone pg--0693 T3, mRNA sequence.
                                                                                                                                                                                                                                                      Bombyx mori
                                                                                                                                                                                                                                                                                                                              AV404200.1 GI:6908288
                                                                                                                                                                                                                                                                             domestic silkworm.
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Research Group
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/dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Irradiated"
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Pred. No. 1e-107;
Pred. No. 1e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TTTGGCAATATCAACCGCACGGCCTGTACCATGGCAATCTCTGCATCTTGCCCCCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGGCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACTTGCAGTACCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c9c99cactac99caataatccgcataagcgaatgttgcgagcacttgcagtacctttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTCCCCCACAGCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atagoogacgcctttgcatcttccgcactctttctcgacaactctcccccacagctctgt 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | gtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtgggttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATATGCTGCGCCTTGCTGGCATCCTTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99taaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatccttga 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGGTTG
Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Clo
Dvorak,J., Fenton,R.D., Gustafson,P., Han,P.S., Hsia,C.C.,
Kianian,P., Lazo,G.R., Miller,R., Otto,C., Nguyen H.T., Rau
                                                                                                                                                                                                                                                  BG312470 373 bp mRNA EST 23-FEB-2001 WHE2408_F10_L20ZS Wheat 3-6 DAP seed cDNA library Triticum aestivum cDNA clone WHE2408_F10_L20, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382;
                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                bread wheat.
Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nirs.go.jp
                                                                                                Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method:uni-directional, sequence direction:sequenced from T3 primer
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                                                                           (bases 1 to 373)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
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newly-eclosed adult"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"
211 c 185 g 218 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone="pg--0693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bombyx mori"
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                                             Close, T.J.,
                         Kang, Y.,
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Best Local Similarity
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                       361 CGAAGTGACCAAC 373
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                                                                                                                    cccgctttcacgaaggtcatgtgtaaaaggccgcagcgtaactattactaatgaattcag 95
                                                       cgaagtgaccaac 408
                                                                                                TTCGGGATTGCATTTTGCAGACCTCTCTGCCTGCGATGGTTGGAGTTCCAGACGATACGT 360
                                                                                                                                                                         GTGCAGATATAAAAAATCCCGAAACCGTTATGCAGGCTCTAACTATTACCTGCGAACTGT 300
                                                                                                                                                                                               gtgcagatataaaaaatcccggaaaccgttatgcaggctctaacctattacctgcgaactgt 335
                                                                                                                                                                                                                                                                    gcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctcttacctgtt 275
                                                                                                                                                                                                                                                                                                                                                             tacgcatttggtgatccggttctgcttccggtattcgcttaattcagcacaacggaaaga 215
                                                                                                                                                                                                                                                  GCACTGGCTAACCAGGCTCGCCGACTCTTCACGATTATCGACTCAATGCTCTTACCTGTT 240
                                                                                                                                                                                                                                                                                                                                                                                                       GACAGACAGTGGCTACGGCTCAGTTTGGGTTGTGCTGTTGCTGGGCGGCGATGACGCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCGCTTTCACGAAGGTCATGTGTAAAAGGCCGCAGCGTAACTATTACTAATGAATTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence have been trimmed to remove vector sequence quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the wheat genomes - 3-6,DAP seed cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, GA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5105595818
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a .93 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Total RNA was prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Wheat 3-6 DAP seed cDNA library"
/tissue_type="Young seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Pred. No. 1.8e-103;
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GCACTGGCTAACCAGGCTCGCCGACTCTTCACGATTATCGACTCAATGCTCTTACCTGTT
                         gcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctcttacctgtt 275
                                                                                                                                                                                                                                                                         gacagacagtggctacggctcagttttgggttgttgctgtttgctggggcggatgacgccctg 155
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1 (bases 1 to 498)
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The ABI trace of this sequence can
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//lab_host="E. coli XIJ-Blue"
//lab_host="E. coli XIJ-Blue"
//note="vector: lambda2apII (UniZap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNAse H and DNApol I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
Center, Smith College, Northampton, MA 01063 USA phone +1
413 585 3826, fax +1 413 585 3786 email genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Brugia malayi day 6 post-infection third stage
larvae SAW96MLW-BmL3d6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
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1 (bases 1 to 399)
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Shoujing Road, Zhangjiang
Location/Qualifiers
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XhoI"
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/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="NPCDBD10"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RETWORDS SOURCE SOURCE ORGANIS REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUR BASE COUN	RESULT AR13837; LOCUS LOCUS DEFINIT: ACCESSIO		44 42 44 44 45	. 3 3	36 37	34 354	မ သ သ	30 31	28 29	26 27	24	22	20	18	16 17	14 15	13	111	9 10	. 8	6 7	4 7	- ω	1 2	
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Unknown. Unknown. Unclassified. Unclassified. 1 (bases 1 to 1. Couto, L.B., Colo, Adeno-associated target cells patent: US 62005 Locatio 1, 119 /organi 3258 a 2818	38377 uence 1 38377 38377.1		41.4 41.4 41.4 41.4 37.2	44.3	44.3			51.7 51.7	51.7 51.7	51.7	56.8	57.2 57.0	س بر	ωw	ωω	4 5	i Ci C	лО	U) U	ı un	7	7 0	72.5	00	
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661 aacatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgag
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                                                                                                                                                                                                                                                                        361 TGCGTGCCTTGAATTACTGACACTGACATCCACTTTTTCTTTTTTCTCCACAGGTATCGAT
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                                               ttcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc 660
                                                                                                          gatctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca
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                               TTCAACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTC
                                                                                          GATCTCGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCA
                                                                                                                                                     AGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGT
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Couto,L.B., Colosi,P.C. and Qian,X.
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Sequence 13 from patent US 6221349.
AR146887
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                                                                                                      186 GATGTCGTGTACTGGCTCC---GCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGT
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291 CGGCAGGTAAGTGCCAGGGAATGTTTGTTCTTAAATACCATCGCTCCAGGGAATGTTTGT 350
             301 aggcaggtaagtgccgtgtgtgggttcccgcggggcctggcccttttacgggttatggccct 360
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                                                 GCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTT-----TGCCGCCCCG 290
                                                                   aaagaagtatattagagcgagtctttctgcacacagatcacctttccgggtgccgccct 300
                                                                                                                                                        859;
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Couto, L.B., Colosi, P.C. and Qian, X.
Adeno-associated virus vectors for expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            target cells
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Pred. No. 6.7e-210;
0; Mismatches 118; Indels 23;
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Local Similarity 85.9%;
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Couto, L.B., Colosi, P.C. and Qian, X.
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Voorberg, J.J
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                                                                                                                                      Sequence 1 from patent US
AR112722
                                               Hybrid proteins with modified activity Patent: US 6130203-A 1 10-OCT-2000;
                                                                                                                                                          AR112722
                                                                  Voorberg, J.J
                                                                                                Unknown
                                                                                                          Unknown.
                                                                                                                            AR112722.1 GI:14092622
                                                                                      Unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 ATCTCGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCAT
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synthetic construct
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                                                                                                                                              Patent: WO 8809813-A 7 15-DEC-1988;
                                                                                                                                                                                artificial
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                                                                                                                                                                     (bases 1 to
                                /codon_start=1
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                     translation="mQIELSTCFFLCLLRFCFSATRRYYLGAVELSWDYMQSDLGELP
                                                                                                  /organism="synthetic construct"
/db_xref="taxon:32630"
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Query Match Best Local : 366 TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG 246 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545 426 catgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgctttagtgc 485 66 CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 125 6 CATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTGCGATTCTGCTTTAGTGC 65 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGT tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttccatgctgt 785 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT 245 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665 CGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAA 185 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa 605 57.5%; Score 575; DB 6; Length 8241; Similarity 100.0%; Pred. No. 5.1e-164; 2625 a RPOLHESGONVETERSGIOLELANGELE FENDALESCHANDELE FALLESCHANDELE IN PROLHESGONVETERSGIOLE IN ROTUNTSSUAPESGIOLELANGE LEGITATELE KETTATELE KATETATELE KETTATELE K LQVDBÖKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY" NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW TYRGNSTGTLMVFFGNVDSSG1KHN1FNPP11ARY1RLHPTHYS1RSTLRMEWMGCDL VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWR YEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYED SYEDJSAYLLJSKNNALEPRSFSONSRHPSTROKOFNATTIPENDIEKTDPWFAHRTPM PKIONVSSSDLLMLLROSPTPHGLSLSDLQEAKYETFSDDPSPGAIDSNNSLSEMTHF PEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMY  ${\tt RLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNMERDLASGL}$ VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVREMAY TDETEKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGITDVRPLYSR IGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAGVQLED QHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRS AVFDEGKSWHSETKNSLMODRDAASARAWPKNHTVNGYVNRSLPGLIGCHRKSVYWHV IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF 1759 c Mismatches 1703 g 0; Indels 0; Gaps 425 365

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Van Ooyen, A.J., Andreoli, P.M., Van Mourik, J.A. and Pannekoek, H. Method for the preparation of proteins with factor VIII activity microbial host cells; expression vectors, host cells, antibodies patent: EP 0253455-A 23 20-JAN-1988;
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                                                                           KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
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EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
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ENTVLPKPDLPKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGSLLQGTEGAI
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RLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNWERDLASGL
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QHDGWBAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSOYLNNGPQRIGRKYKKVRFMAY
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KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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/db_xref="GI:412968"
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                                                                                                                                                                                                                                                                                                        TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 580
                                                                                                                                                                                                   Complete cDNA encoding human factor VIII
              Danieru,J.K., Richiyaado,M.R., Goodon,A.B. and Uiriamu,A.U. MANUFACTURE OF FUNCTIONAL VIII FACTOR Patent: JP 1985243023-A 2 03-DEC-1985;
                                                              Mammalia; Eutheria; Primates; 1 (bases 1 to 8831)
                                                                                                                   Homo sapiens
                                                                                                                                                  E00527.1 GI:2168806
JP 1985243023-A/2.
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Patent: JP 19
                                                                                                                                     Homo sapiens.
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IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETYEMLPSKĄGIWR
VECLIGEHLHAGMSTLFLYYSNKOQTPLGMASCHIRDFQITASGQYGQWAPKLARLHY
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100.0%; Pred. No. 5.1e-164;
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PD 03-DEC---
PF 19-APR----
PR 20-APR---
PI DANIERU
AREN BIHAAN
PI UIRIAMU
PC 612N5/0
PC C12N5/0
PC C12N5/0
CC 12N5/0
CC topolog
CC hypothe
CC anti-se
CC *source
CC *source
FH Key
FT 5'UTR
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                                              TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG
                                                                                          CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 408
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03-DEC-1985
19-APR-1985 JP 1985085295
20-APR-1984 US 84 6023
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Key Location/Qualifiers
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/db_xref="taxon:9606"
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100.0%; Pred. No. 5.2e-164;
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7266. .<8967
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110. .7265

 Mismatches

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TITLE
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1 (bases 1 to 8967)
Saenko,E.L. and Strickland,D.K.
Methods of reducing factor viii clearance and compositions therefor Patent: WO 0071714-A 1 30-NOV-2000;
The American National Red Cross (US)
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ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
DYGMSSSPHVLRNRAQSGSVPQFKKVVPQEFTDGSFTQPLYRGELNEHLGLLGPYIRA
TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
                 VECLIGEHLHAGMSTLFLVYSNKCQTFLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ
                                                    IFDETKSWYFTENMERNCRAPCNIOMEDPTFKENYRFHAINGYIMDTLPGLVMAODOR
IRWYLLSWGSNENIHSJHFSGHVFTVRKKEEVKMALYNLYPGVFETVEMLPSKAGIWR
                                                                                       EVEDNIMVTFRNQASRPYSFYSSLISYEEDOROGAEPRKNFVKDNETKTYFWKVOHHM
APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
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/db_xref="GI:12226921"
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BASE COUNT
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171409
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                              1 (bases 1 to 8967)

Bodner,M., De Polo,N.J., Chang,S., Hsu,D.Chi-Tang and Respess,J.G. Retroviral delivery of full length factor VIII

Patent: US 5681746-A 1 28-OCT-1997;
Location/Qualifiers
                                                                                                                                      Unknown
                                                                                                                                                     Unknown.
                                                                                                                                                                                                  Sequence 1 from patent US 171409
                                                                                                                          Unclassified.
                                                                                                                                                                                  I71409.1 GI:3007544
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∕organism="unknown"
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LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
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Pred. No. 5.2e-164;
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                                                                                       FEATURES
                                                                                                      COMMENT
                                                                                                                                                                                  AUTHORS
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                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          666 cyctaagccaaggccaccotggatgggtctgctaggtcctaccatccaggctgaggttta 725
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                                    misc_feature
                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG 528
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                                                                                                                           Wood, W.I., Capon, D.J., Simonsen, C.C., Eaton, D.L., Gitschier, J., Keyt, B., Seeburg, P.H., Smith, D.H., Hollingshead, P., Wion, K.L., Delwart, E., Tuddenham, E.G.D., Vehar, G.A. and Lawn, R.M. Expression of active human factor VIII from recombinant DNA clones Nature 312 (5992), 330-337 (1984)
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                     Human mRNA for factor VIII.
                                                                                                                                                                                                                                                                                                                   HSFVIIIR
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 8967)
                                                                                                                                                                                                                                                              factor VIII; signal peptide.
                                                                                                                                                                                                                                                                            X01179.1 GI:31498
                                                                                                      Data
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                                                                                                      kindly reviewed (20-MAR-1986) by W. Wood
            /note="5' untranslated region" 110. .166
/product="signal peptide (aa -19 to -1)"
                                                                                        Location/Qualifiers
                                                 /db_xref="taxon:9606"
                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                   8967 bp
                                                                                .8967
                                                                                                                                                                                                                                                                                                                      mRNA
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Matches
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546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                                 169 CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
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VAKKHPKTWVIY I AABEEDWDY AP LULAD DDDRSYKSQULNUGOPORIGERKYKKVERPMAY
VAKKHPKTWVIY I AABEEDWDY AP LULAD DDRSYKSQULNUGOPORIGERKYKKVERPMAY
TDETFEK FREATOHESGILIGPLLYGEVGDTLLI IF KNOASRPYNIY PHGITDVRPLYSR
TDETEK FREATOHESGILIGPLLYGEVGDTLLI IF KNOASRPYNIY PHGITDVRPLYSR
TDETEK FREATOHESGILIGPLLYGEVGDTKEND FREATOHEARTH
RLPKGVKHLKDFP I LPGEIFKYKWFYUNDGPFKSDPRCLTRY YSSFVNUSEDLASGL
RLPKGVKHLKDFP I LPGEIFKYKWFYUNDGFFKSWILTENOATHELWAYOVLED
IGPLLICYKESVDORGNOIMSDKRINGILIG SUPPLSVFE SGYTKKKMV
PEFOASIUMHSI NGVYPDSLOLSVCLLEVAKWY I LS IGAQTDFLSVFE SGYTKKMV
PEFOASIUMHSI NGVYPDSLOLSVCLLEVAKWY I LS IGAQTDFLSVFE SINLI ST INSLINGATUR
SYEDISANLINGSUK I PEPAANIPH SKE SEFTEDDFS ARIONSKLISSGLE SHTHF
NGOASINGKNVSTESGRELF KGKARAHGPALLTRONALFKVS I SLLKT NKTS NNSATUR
NGOESGNOK NVSSTESGRELF KGKARAHGPALLTRONALFEVS I SLLKT NKTS NNSATUR
NGOESGNOK NVSSTESGRELF KGKARAHGPALLTRONALFEVS I PEDAANIPH SKE SEFTENDEN SKE SKENTI I SPWT
YAPVLODFRS LINDSTURTKKHTAHFSKKGEEENLEGLGOPKO I USEKKACTTT I SPWT
YAPVLODFRS LINDSTURTKKHTAHFSKKGEEENLEGLGOPKO I SKRKAKLT PST LTO IDV NE
SOONWYTORSK RALKOFALD-LEEFTELEKRI I VDDTSTOWSK NNKHLT PST LTO IDV NE
SOONWYTORSK RALKOFALD-LEEFTELEKRI I VDDTSTOWSK NNKHLT PST LTO IDV NE
SOONWYTORSK RALKOFALD-LEEFTELEKRI I VDDTSTOWSK NNKHLT PST LTO IDV NE
SOONWYTORSK RALKOFALD-LEEFTELEKRI I VDDTSTOWSK NNKHLT PST LTO IDV NE
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SOONWYTOR KRALKOFALD-LEFTELEKRI I VDDTSTOWS KNKKLT PST LTO IDV NE
SOONWYTOR K
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VDARFEPPRVFKSFFNTSVVYKKTLFVEFTDHLFNILGALLVCREGSLAKEKTOTLHKFILLF
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTOTLHKFILLF
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/db_xref="GI:31499"
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QHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSESFIQIRS
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DYGMSSSPHULRURAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELUEHLGLLGPYIRA
EVEDULIWTFRNQASRPYSFYSSLISYEEDQRQGAEPRKUFVKPUETKTYFWKVQHHM
APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTUTLUPAHGRQVTVQEFALFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="mature factor VIII (aa 1-2332)"
7163. .8967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGOYGQMARKLARHHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLVISQFIIMYSLDGKKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYIMDTLPGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="polyA_site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="polyadenylation signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 575; DB 9; L
100.0%; Pred. No. 5.2e-164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 tgtggacctggtaaaagacttgaattcaggcctca 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726 tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgt 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT 348
Draft entry and clean copy sequence for [1] kindly provided by M.A.Truett, 26-FBB-1996.
The mutation at position 1042 results in a change of Glu to Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99agaaagaagatgataaagtottocotggtggaagcoatacatatgtotggcaggtoot 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG
                                                                                                                                     88197150
                                                                                                                                                                   DeRosa, V. and Marchetti, G. A HindIII RFLP and a gene lesion in the coagulation factor VIII
                                                                                                                                                                                                                 g (sites)
Bernardi,F., Legnani,C., volinia,S., Patracchini,P., Rodorigo,G.,
                                                                                                                                                                                                                                                                                    Moderately severe hemophilia A resulting from Glu----Gly substitution in exon 7 of the factor VIII gene Am. J. Hum. Genet. 42 (6), 867-871 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgctaagccaaggccacctggatgggtctgctaggtcctaccatccaggctgaggttta 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGAGCTGCCTGTGGA GCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAA 288
                                                                                                                                                                                                                                                                                                                                                                    Youssoufian, H., Wong, C., Aronis, S., Platokoukis, H., Kazazian, H.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization of the polypeptide composition of human factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Truett, M.A., Blacher, R.W., Burke, R.L., Caput, D., Chu, C., Dina, D., Hartog, K., Kuo, C.H., Masiarz, F.R., Merryweather, J.P., Najarian, R. Pachl, C., Potter, S.J., Puma, J., Quiroga, M., Rall, L.B., Randolph, A. Urdea, M.S., Valenzuela, P., Dahl, H.-H.M., Favalaro, J., Hansen, J., Nordfang, O. and Ezban, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIII:C and the nucleotide sequence and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 to 9029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coagulation factor VIII:C. Human kidney, cDNA to mRNA, clones pF8[100,102]; and cell line GM1416 DNA, clone pF8-4.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMFVIIIC 9029 bp mRNA PRI (Human coagulation factor VIII:C mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cidney cDNA
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                                                                                                                                                                                                                                                                                                                                                               and Antonarakis, S.E.
                                                                                                                                          Genet. 78 (4), 359-362 (1988)
                                                                           sites; mutations causing hemophilia
                                                                                                sites; mutation causing hemophilia
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variation

6853

/gene="F8C"

/gene="F8C"

/note="a in wt; g in hemophiliac [2]"

/note="g in wt; a in hemophiliac [2]"

/gene="F8C"

variation

variation

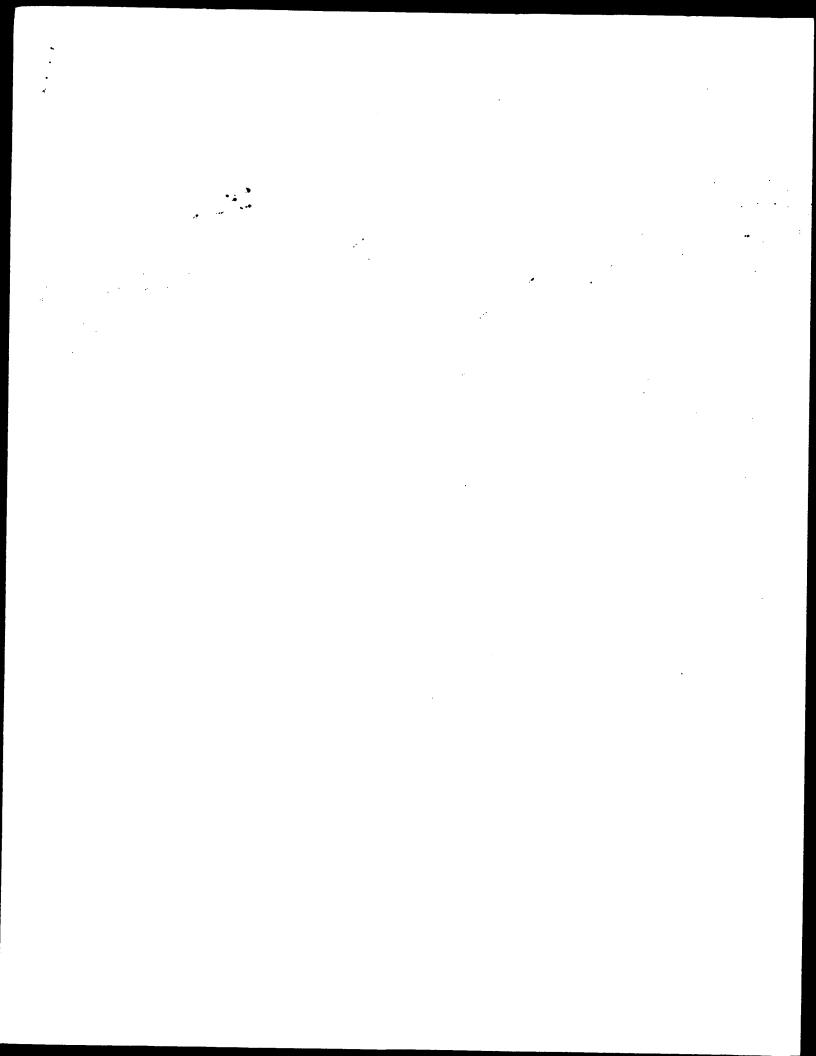
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OHGMEAV KYNDECPERPOLEMKNIEE ALKTHE LIAVITLAMDLGUPLLINCHISH OHDGRAVY KYNDECPERPOLEMKNIEE AERDY DDELTDSEMDVREDDINGPSETOIRS VAKKHEKTWOHY I AAEEEDMDY APLVLAPDDRSY KSQYLINIGPORI GRRYK KYREMAY TDETFKTREALQHESGI LGPLLY GEWGDTLLI I FK NQASRPYNIY PHGITDVRPLY SR TDETFKTREALQHESGI LGPLLY GEWGDTLLI I FK NQASRPYNIY PHGITDVRPLY SR RLPKGYKHLKDP FLIPGEI FKY KWYTVEDBOFTKSDPROLTRY Y SSFVINIEDLY SR I GPLLI CYKRESVDOBGNQI MSDKRIVI LIFS VPDERRSWYLTENI GOFTLENDRACYOLED PEGASI I MHS I NGYVFDSLOLS VCLHEVAY WYLLSI CAOTDPLS VFPSGY TPKHKIV Y PDTILTLE PPSGETYWRSKEN PGLINGLONG TOR ALKT TIPENDI EKTOPWFARTT PK Y Y PDTILTLE PPSGETYWRSKEN PGLINGLONG TOR ALKT TIPENDI EKTOPWFARTT PK Y Y PDTILTLE PPSGETYWRSKEN PGLINGLONG TOR ALKT TOR ALKT TOR ALL XY SCOKINGLONG Y PED PK LONVYSSODLAMLI CORPT PHGLSLDLOLAKKET FSDDE SPRAILI STIP SDNLA NSOESWOKN VSTETSGDLE KREKT FF TRAFTEN AGTINTS SLOPEN PHOLALIR KYTTAATELK KLDFK VSSTSUNLI STIP SDNLA NSOESWOKN VSTETESGICH LKEKET FTAATELK KLDFK VSSTSUNLI STIP SDNLA NSOESWOKN VSTETESGICH FKOKRAHGPALLT KONALFKY VSTSULLTENGE YNG PROLITE SKINEN VOOR KEGD I PPDAQNPDMSFFKMLF LJSTRONKESYDOA YAPVLODERSLID PED PADANPDMSFFKMLF LJSTRONKESYDOA YAPVLODERSLINGT PED PADANPDMSFFKMLF LJSTRONKESYDOA SQONFYTORSKKAL KORT KYRT SHOLST TIP SDNLA YAPVLODERSLINGT KHTAH SKKGEEENLEGLGUOTKOI VEKY ACTTRISPNT SKRIGAT STORYKESYDOA SQONFYTORSKKALKORELD FEETELK KI I VDDTSTOWSKINK HLTPSTLTOI DYNE AASY KKOSG VOESSHFOGAKKNINGLA LITLEMTGDDREWGLGT SATINSYTYKKY KWNEANNES LYDGAKKNINGLA LIFLEMTGDDREWGLGT SATINSYTYKKY KWNEANNES KOFT STORYKESALI
                                                                                                                                                                                                                                                                                                                                                APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
IFDETKSWYETENNERNCRAPCNIQMEDPTFKENYRFHAINGYIMTLPGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETYEMLPSKAGIWR
                                                                                                          DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY'
                                                                                                                                             NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW
LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
                                                                                                                                                                                                                             TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
                                                                                                                                                                                                                                                                         VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWNEANRPCKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
DYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELMEHLGLLGPYIRA
note="coagulation factor VIII:C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVEDNIMVTERNQASRPYSEYSSLISYEEDQRQGAEPRKNEVKPNETKTYFWKVQHHM
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IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH
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VYITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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/db_xref="GI:182818"
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172. .228
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172. .7227
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                                                                  1 (bases 1 to 7272)
Sarver, N. and Drohan, W.
Factor VIII-C analogs
Patent: EP 0265778-Al 3 04-MAY-1988;
Location/Qualifiers
                                                                                                                                                        Sequence 3 from Patent EP 0265778
                                                                                                               Unclassified
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                                           /organism="unknown"
1591 c 1533 g
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100.0%; Pred. No. 5.2e-164;
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Search completed: January 8, 2002, 17:15:54 Job time: 12045 sec



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OM nucleic - nucleic search, using sw model
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 5 5 6 7 7 7 10	Result No.	
1000 1000 725.2 725.2 725.2 617.4 577.4 577.8 575.8 575.8	Score	
100.0 11933 21 AAD00121 100.0 11933 22 AAD08612 72.5 4999 21 AAD08613 72.5 4999 22 AAD08613 72.7 7944 22 AAF84647 57.7 12445 21 AAA49232 57.6 11846 20 AAX82250 57.6 11846 20 AAX82250 57.6 12022 20 AAX82260 57.5 4832 19 AAV19581	Query Match Length DB ID	d
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plasmid DLZ/ encod	Homo sapiens facto	Human Factor-VIII	DNA encoding /40 A	-	Modified factor VI		Beta-domain detece	cDNA encoding liulia	Sequence encoding	B-domain deleted F	Homo sapiens facto	Human Factor VIII	Sequence of human	DNA construct HSV/	Human factor VIII		Human factor VIII	Factor VIII:C (Arg	Human Factor VIII	Factor VIII:C codi	Human Factor VIII-	factor		factor	Human full-length	Human factor VIII	Human factor VIII	Factor-VIII full-1	cDNA sequence enco	Factor VIII cDNA i	Human Factor VIII Factor-VIII cDNA.	TTTV CLEAN VITT

## ALIGNMENTS

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AAD00121
                                                                                                            AAD00121 standard; DNA; 11933 BP.
                                                                                                     AAD00121;
                                                                                             31-JUL-2000 (first entry)
                                                                                     Recombinant adeno associated vector construct, pAAV-F8-1.
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Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII; hFVIII; HNF-3 albumin promoter; human elongation factor-lalpha; EF1alpha; human growth hormone; hGH; inverted terminal repeat; ITR; haemophilia; human growth hormone; hGH; inverted terminal repeat; gene therapy; ds.

Adeno associated virus.

WO200023116-A1

27-APR-2000. 19-OCT-1999; 99WO-US24495.

20-OCT-1998; 24-MAR-1999; 30-JUL-1999; 98US-0104994. 99US-0125974. 99US-0364862

(AVIG-) AVIGEN INC.

Couto LB, Colosi PC;

WPI; 2000-339536/29

New recombinant adenovirus-associated vector, useful for gene therapy

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В
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601 ttcaacacctcagtcgtgtagcaaaaagactctgtttgtagaattcacggatcaccttttc 660
                                            541 gatctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca
                                                                   541 gatctoggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca 600
                                                                                                                             481 agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrvIII coding region comprises the heavy chain gene segment with the and 5 amino acids from the N-terminus of the B domain. All and A2 domains segment comprises the c-terminal 85 amino acids of B domain and the A3, into the same plasmid seperated by 42 nucleotides coding for 14 residues control sequences, that directs the transcription and translation of the B domain, that is deleted. This plasmid is operably linked to factor VIII gene. The adeno-associated viral vectors are used for gene therapy, because of their broad host range, safety profile and duration of the range of the same philia. This method allows prolonged expression of the therapy, because of their broad host range, safety profile and duration
                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 aaagaagtatattagagcgagtétttctgcacacagatcacctttccgggtgccgccct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-lalpha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII) and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 tttggtcgcccggcctcagtgagcgagcgcgcgcagagagggagtggccaactccatc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 5; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
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                                                                                                                                                      agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540
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suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprises a nucleotide sequence encoding the light chain of factor VIII and a second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is

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                                        The present invention relates to a method for treating a subject
                                                                                          administering recombinant adeno-associated vectors which express blood coagulation factor \mathtt{VIII} .
                                                                         Claim 18; Fig 5; 90pp; English
                                                                                                               Treating blood clotting disorder, especially hemophilia in mammals, by
                                                                                                                                                                        Couto LB, Colosi PC, Qian X;
                                                                                                                                                     WPI; 2001-417955/44.
                                                                                                                                                                                                    (AVIG-) AVIGEN INC
                                                                                                                                                                                                                           22-DEC-1999;
                                                                                                                                                                                                                                               21-DEC-2000; 2000WO-US34925.
                                                                                                                                                                                                                                                                                                                  Chimeric - Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                      Chimeric - Adeno associated virus.
                                                                                                                                                                                                                                                                                                                                                                                   blood clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                              Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
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Pred. No. 9.8e-278;
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         The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct pVm4.1cp8deltaB. This expression vector comprises the CC promoter, first intron (-573 to +995) of human elongation factor-lalpha CC promoter, first intron (-573 to +995) of human elongation factor-lalpha CC promoter, first intron (-573 to +995) of human elongation factor-lalpha CC polyadenylation signal from human growth hormone (hGH). This sequence is CC polyadenylation signal from human growth hormone (hGH). This sequence is CC first 57 by encoding the 19 amino acid signal peptide, Al and A2 domains CC and 5 amino acids from the N-terminus of the B domain. The light chain CC and 5 amino acids from the N-terminus of the B domain and the A3. CC segment comprises the C-terminal 85 amino acids of B domain and the A3. CC control sequences, that directs the transcription and translation of the CC control sequences, that directs the transcription and translation of the Factor VIII gene. The adeno-associated viral vectors are used for gene CC therapy to treat haemophilia. This method allows prolonged expression of therapy, because of their broad host range, safety profile and duration of expression in the infected hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant Adeno Associated Vector; rAAV; pVm4.1cf8deltaB; promoter; human Factor VIII; hFVIII; EFlalpha; human elongation factor-lalpha; human growth hormone; hGH; ITR; inverted terminal repeat; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; ds.
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24-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                   Example 9; Fig 6; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      operably linked to control sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant adenovirus-associated vector, useful for gene therapy to treat hemophilia, comprises at least a portion of Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AVIG-) AVIGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 gcagtagtcgccgtgaa&gttctttttcgcaacgggtt-----tgccgccccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 aaagaagtatattagagcgagtctttctgcacacagatcacctttccgggtgccgccct 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 gatgtcgtgtactggctcc---gcctttttcccgagggtggggggagaaccgtatataagt 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 actaggggttcctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                      gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt
                                                                                                                                                     Match
                                                                                                                                                                                                          gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 829
                                                                                                                                                                                                                                9ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
                                                                                                                                                                                                                                                                                                           9tttatgatacagtggtcattdcactttaagaacatggcttcccatcctgtcagtcttcat 780
                                                                                                                                                                                                                                                                                   gittatgatacagiggicattacacitaagaacaiggcitcccaiccigicagicitcai 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttcaacacetcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gatctcggtgagctgcctgtggacgcahgatttcctcctagagtgccaaaatcttttcca
                                                                                                                                                                                                                                                                                                                                                                                                                                       ttcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaagatttttcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tocaccatgcaaatagagctotccacctgcttctttctgtgcctttttgcgattcttgcttt 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tccaccatgcaaatagagctctctacctgcttctttctgtgcctttttgcgattctgcttt 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt tcttaaataccatctact} {\tt gacactgacatccactttttctttttctccacaggtatcga-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgcgtgccttgaattagtgacactgacatccacttttttctttttctccacaggtatcgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cggcaggtaagtgccagggaatgtttgttcttaaataccatcgctccagggaatgtttgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggcaggtaagtgccgtgtgtggttcccgcgggcctggcctctttacgggttatggccct 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgttcttaaataccatccagggaatgtttgttcttaaataccatctacagttattggtt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actaggggttcctgcggccgcacgcgtggtggcgcggggtaaa-----ctgggaaagt 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttggtcgcccggcctcagtgagcgagcgcgcgcagagagggagtggccaactccatc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagctgcgcgctcgctcactgaggccgcccgggcaaagcccgggcgtcgggcgacc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tttggtcgcccggcctcagtgagcgagcgcgcgcgcagaggggagtggccaactccatc 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 1375 A; 1351 C; 1155 G; 1318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 725.2; DB 21; Length 4999;
Pred. No. le-198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches, 118; Indels 23; Gaps
                                                                                                                                   889
                                                                                                                                                                                                                                                                                                                                                                                                                                             649
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QΥ DЪ Ş 밁 Q В δÃ DЬ δ 밁 Ş В οy 밁 Ş B γQ В Qγ В Š 밁 δÃ 뫄 Qy 문 δõ 맑 Qy Ъ

Qy Дb ΩV DЬ

121 actaggggttcctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgt 180

73 tttggtcgcccggcctcagtgagcgagcgagcgcgcagaggggagtggccaactccatc

tttggtcgcccggcctcagtgagcgagcgagcgcgcagagaggggagtggccaactccatc 120 cagctgcgcgctcgctcactgaggccgcccgggcaaagcccgggcgtcgggcgacc 72 Ωy

1 cagetgegegetegetegeteaetgaggeegeeegggeaaageeegggegtegggeee

Matches 859; Query Match

Local

Similarity

72.5%; 85.9%;

Score 725.2; DB Pred. No. 1e-198;

DB 22;

Length 4999;

Conservative

0; Mismatches 118; Indels

23; Gaps

4

60

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The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is sequence encoding the heavy chain of factor VIII. The rAAV vector is cuseful in gene therapy for treating haemophilia A in mammals, in particular humans. The rAAV vector provides high level and long term compression of biologically active clotting factor VIII in vivo. The present sequence is pVm4.1cF8-B vector without the plasmid backbone. It comprises human elongation factor 1 (EF1) promoter, and AAV inverted terminal repeats (ITRS) at the ends. The vector cand AAV inverted terminal repeats (ITRS) at the ends. The vector concess both the light and heavy chains of human factor VIII coding sequence, a poly A signal codes both the light and heavy chains of human factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD08613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЪ
Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Fig 6; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood coagulation factor VIII \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-417955/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVIG-) AVIGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens
Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 blood clotting disorder; gene therapy; haemophilia A; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200145510-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Adeno associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pVm4.1cF8-B; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human factor VIII expressing rAAV vector pVm4.lcF8-B partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD08613 standard; DNA; 4999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD08613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         950 tctcatgtggacctggtaaaagacttgaattcaggcctca 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0470618
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133 actaggggttcctgcggccgcacgcgtggtggcgcgggggtaaa-----ctgggaaagt 185

1 1111 1

Synthetic

actagggqttcorron

181 ttgttcttaaataccatccagggaatgtttgttcttaaataccatctacagttattggtt 240

gatgtcgtgtactggctcc---gcctttttcccgagggtgggggagaaccgtatataagt 242

80 망

aggcaggtaagtgccgtgtgggttcccgcggggcctggcctctttacgggttatggccct 360

tgcgtgccttgaattactgacattgacatccactttttctttttctccacaggtatcgat 420 cggcaggtaagtgccagggaatgtttgttcttaaalaccalcgctccagggaatgtttgt 350

tettaaataeeatetaetgaeaetgaeateeaetttttettttteteeaeaggtatega- 409

tccaccatgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgcttt 480 tocaccatgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgctt 469

186

В õ

Š 밁

> 361 291 301

밁

351

QY 멍 Q

410

481 agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540

agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 529

541 gatotoggtgagotgcotgtggacgcaagatttoctcotagagtgccaaaatcttttoca 600

gatotoggtgagotgootgtggaogcaagatttootootagagtgooaaaatottittooa 589

601 ttcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc

ticaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc 649

661 aacatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgag 720

gtttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcat 769

밁 ρ

20 В

Q В

밁 δÃ В

20

δÃ 밁

961 tctcatgtggacctggtaaaagacttgaattcaggcctca 1000

totoatgtggacotggtaaqagacttgaattoaggcotoa 989

890 gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt

gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt 960  781 gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840

gctgttggtgtatqctactggaaagcttctgagggagctgaatatgatgatcagaccagt 829

В 8 В

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DXX PXX X PX
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                              204
                                                                                          рЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200127303-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one encoding B-domain deleted factor vIII operably linked with at least one encoding B-domain deleted factor. The method results in the production enhancer and at least one promoter. The method results in the production of high titer raAv vector stocks carrying the B-domain deleted factor vIII transgenes and expression cassettes, which generate adequate titers virus for in vivo administration. The recombinant vectors are useful of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded for treating haemophilia A, where the liver expresses the blood. They are B-domain deleted factor VIII. which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred expression control element .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walsh CE, Chao H, Burstein H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000; 2000WO-US28221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB67959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-273781/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 64; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a recombinant adeno-associated virus (rAAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
            124 aggggttcctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgtttg 183
                                                                                                                                                                                                                                                                                                               Local Similarity
les 783; Conserv
                                                                                       15 ctgcgcgctcgctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggcttt 74
                                                                                                                                                                                                                              4 ctgcgcgctcgctcgctcactgaggccgcccgggcaaagcccgggcgtcgggcgaccttt 63
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0158780
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150..278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4840..4914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "TK polyA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= C
/note= "human B-domain deleted factor VIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420..4835
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                                                                                                                                                                                                                                                                                                                                                   61.7%; Score 617.4; DB 22; Length 7944; 78.5%; Pred. No. 1.4e-167;
----cagatctctttctaagtaaacagtacatgaaccttt 180
                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                       Mismatches 196;
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                                                                                                                                                                                                                                                                                                                                                      Indels 18; Gaps
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XGXAX
XXXX
                                                                                                 AAF84647 standard; DNA; 7944 BP
                                     Plasmid DLZ6 encoding human :B-domain deleted factor VIII.
        coagulation disorder; ss.
                  Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
                                                            29-JUN-2001
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                                                              (first entry)
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AAT69811
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Homo sapiens
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      blood clotting; procoagulant; anticoagulant; antithrombotic;
haemophilia; gene therapy; ss.
                                    Factor VIII-db695-HCII; heparin cofactor II; blood coagulation;
                                                                        Factor VIII-dB695-HCII DNA
                                                                                                     10-AUG-1997 (first entry)
                                                                                                                                                     AAT69811;
                                                                                                                                                                     AAT69811 standard; DNA; 5035 BP.
                                                                                                                                                                                                                                                           964 catgtggacctggtadaagacttgaattcaggcctca 1000
                                                                                                                                                                                                                                                                                            957 catgtggacctggtaaaagacttgaattcaggcctca 993
                                                                                                                                                                                                                                                                                                                                                     777 gttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaa 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 aacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaac 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 ctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattc 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 gccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgat 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 gtgccttgaattactgacattgacatccactttttctttttctccacaggtatcgattcc 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 caggiaagigcogigigiggitocogogggoolggoolettiaogggitalggoooligo 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 gctggggcttggccataggccatcagcgca-tgcggatctcagtgtggttttgcaagagg
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330 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg
            722 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg 781
                                                                      662 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg
                                                      270 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg
                                                                                                                                602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 661
                                                                                                                210 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 269
                                                                                                                                                                                           542 atctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccat 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                           total liver cDNA, fusion to sequences encoding Factor VIII aa706-711 and aa737-743, and incorporation of the construct into plasmid pCLB-dB695. The hybrid protein, which can be expressed owing to the HCII acidic region, and can be used to treat blood coagulation disorders such as haemophilia A.
                                                                                                                                                                          150 atcteggtgagetgeetgtggaegeaagattteeteetagagtgeeaaaatetttteeat 209
                                                                                                                                                                                                                                                     482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 541
                                                                                                                                                                                                                                                                                                             422 ccaccatgcaaatagagctotccacctgcttctttctgtgccttttgcgattctgcttta 481
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5035 BP; 1484 A; 1127 C; 1110 G; 1314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a hybrid protein in which amino acids 712-736 of Factor-dB695 (Factor VII de1868-1562) B-domain are replaced by amino acids 51-80 from the acidic region (and potential thrombin-binding site) of human haparin cofactor II (HCII). It was obtd. by PCR with the amplification (see also AMT69812-13) of the HCII acidic region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA molecule (AAT59811) codes for Factor VIII-dB695-HCII (AAW18670), a hybrid protein in which amino acids 712-736 of Factor-dB695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 52-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid Factor VIII with modified activity, comprises region from donor anticoagulant or antithrombotic protein - useful for treatment of coagulation disorders
                                                                                                                                                                                                                                                                                              30 ccaccatggaaatagagctctccacctgcttctttctgtgccttttgcgattctgcttta 89
                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= heparin cofactor II region (aa5]-8])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= Factor VIII-dB695-HCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                 57.7%; Score 577.4;
99.8%; Pred. No. 3.5
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osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral; blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract; haemophilia; ractor VIII; human; transgene; adenosine deaminase deficiency; ss; sickle cell anaemia; thalassemia; diabetes; alpha-antitrypsin deficiency; slckle cell anaemia; thalassemia; diabetes; alpha-antitrypsin defect; hlabelmer's disease; brain disease; heart disease; immune system defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA49232 standard; DNA; 12445 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2000 (first entry) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector HSQReNeo for transforming endothelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962
                                                                                                                                                                                     Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with collagen I coated surface in culture medium comprising vascular
                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200032750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
The invention relates to a method for expanding the population of endothelial cells (EC) obtained from peripheral blood, by culturing, in contact with a collagen I coated surface, buffy coat cells obtained from peripheral mammalian blood in the presence of a culture medium containing vascular endothelial growth factor (VEGF) and free of bovine brain extract. EC are useful for treating hemophilia by introducing it into the blood stream of a mammal, so that an effective amount of Factor VIII protein is secreted in the blood stream of the mammal.
                                                                                                                                                                                                                                              WPI; 2000-412303/35....
                                                                                                                                                                                                                                                                                                                                                                           (MINU ) UNIV MINNESOTA.
                                                                                                                                          Claim 19; Fig 4; 53pp; English.
                                                                                                                                                                           endothelial growth factor
                                                                                                                                                                                                                                                                                                                  (LOLL/) LOLLAR J S.
                                                                                                                                                                                                                                                                                                                                                (HEBB/)
                                                                                                                                                                                                                                                                                                                                                               (UYEM-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fracture; osteoporosis.
                                                                                                                                                                                                                                                                                                                                             HEBBEL R P.
                                                                                                                                                                                                                                                                                                                                                                  UNIV EMORY.
                                                                                                                                                                                                                                                                                 Lin Y, Lollar JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12445 BP; 3255 A; 2989 C; 2951 G; 3250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     1003 acatcyctaayccaayyccaccctygatygytctyctagytcctaccatccayyctyayy
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1303 ctcatgtggacctggtaaaagacttgaattcaggcctca 1341
                                                                             1243 tcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatcttt 1302
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                   962 ctcatgtggacctggtaaaagacttgaattcaggcctca 1000
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99.8%;
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XW XXX
                                                                                                                                 AAX82259
splicing pattern; RNA processing; gene regulation; beta-domain; ss.
                                                                                                                    AAX82259 standard; cDNA; 9164 BP
                  Factor VIII protein; gene modification; gene therapy; clinical disorder;
                                             Beta-domain deleted Factor VIII protein encoding gene (uncorrected).
                                                                      18-AUG-1999
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
1301 tttatgatacagtggtcattacacttaagaacatggcttccccatcctgtcagtcttcatg 1360
                                                                               1241 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 1300
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                     722 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg
                                                                                                      662 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 721
                                                                                                                                                                                 602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 661
                                                                                                                                                                                                                                                                                                                                                 482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9164 BP; 2451 A; 2170 C; 2081 G; 2462 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              422 ccaccatgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgcttta 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patterns, useful for expression of, e.g. beta-domain deleted factor
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Local_Similarity 99.7%;
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                                                                                                                                                                                                                                                                    atctcggtgagctgcctgtggacgcaagatttccttcctagagtgccaaaatcttttccat 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Sequence 11846 BP; 3419 A; 2718 C; 2607 G; 3102 T; 0 other:

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                                                The invention describes novel genes and vectors exhibiting increased expression and novel splicing patterns. It provides a gene encoding a factor VIII protein, that comprises one or more consensus or near consensus splice sites which have been corrected to increase expression. The method, DNA sequences and expression vectors can be used to increase modified 5 and/or 3' untranslated regions have optimized expression levels and tissue-specific expression. The methods are used for introns, aptimization of 5 and 3' untranslated regions and increase in cytoplasmic RNA accumulation. Hence the DNAs are useful in gene therapy regulation. The present sequence represents the full length factor VIII profession and correction of consensus the full length factor VIII profession and correction of consensus the full length factor VIII profession and correction of consensus the full length factor VIII profession encoding gene sequence represents the full length factor VIII profession and correction of consensus which were the sequence represents the full length factor VIII profession and correction of consensus which were the sequence represents the full length factor VIII profession and correction of consensus which were the sequence represents the full length factor VIII profession and correction of consensus splice sites.
                                     protein encoding gene sequence (construct pLZ-6). This contains an
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05-DEC-1997;
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                              spanning the beta-domain.
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97US-0067614.
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                                                                                                                                                                                                                                                                                                       AAX82260;
                                                                                                                                                                                                       Factor VIII protein; gene modification; gene therapy; clinical disorder; splicing pattern; RNA processing; gene regulation; beta-domain; human;
                                                                                                                                                                                                                                                  Factor VIII protein encoding gene sequence.
                                                                                                                                                                                                                                                                            18-AUG-1999
                                                                                                                                                                                                                                                                                                                                  AAX82260 standard; cDNA; 12022 BP.
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                            /number= 1
3295..6152
                                                                     1006..3294
                                                                                   /product= "Factor VIII protein"
/note= "contains introns"
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 Mismatches

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes and vectors exhibiting increased expression and novel splicing patterns, useful for expression of, e.g. beta-domain deleted factor
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segment encoding the beta-domain"
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99.7%;
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factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV) expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered intravenously to a human. The long term systemic expression results in a measurable level of the therapeutic protein being produced in the blood of the human for a period of at least 30 days after the administration of
                                                                                                                                            This cDNA encodes the beta domain deleted SQN deletion protein of human
                                                                                                                                                                                                                           New replication defective recombinant retro-viruses - which can be administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable
                                                                                                                                                                                  Example 28; Pages 210-213; 272pp; English.
                                                                                                                                                                                                                                                                                                         P-PSDB; AAW46246
                                                                                                                                                                                                                                                                                                                                                     Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Replication defective; Recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypophtuitarism; adenine deaminase deficiency, HTV infection; anaemia;
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R, Mittelstaedt DM, Prussak CE,
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DC, Ibanez CE;
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                                     Human Factor VIII SQN deletion mutant DNA.
                                                                                                                           AAV15338;
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                                                                                                                                                         AAV15338 standard; DNA; 4832 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RRV vector preparation. RRV's can be used for in vivo delivery of therapeutic protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, hypercoagulable disorders, liver diseases such as hepatitis, disorders such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe combined immunodeficiency (SCID), cystic fibrosis. Duchenne's Muscular Dystrophy, inherited emphysema, familial hypercholesterolemia, such as diabetes, hypopituitarism, adenine deaminase deficiency, alphalantirypsin deficiency, Guacher's syndrome, anaemia, infections such as inflammatory disease or graft versus host disease. RRV's are capable of surviving inactivation in human serum thereby allowing efficient gene transfer over prolonged persons of time.
                                                                                                                                                                                                                                                                                                                                                                                        491 ggagaaagaagatgataaagtottccctggtggaagccatacatatgtctggcaggtcct
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                                                                               (first entry)
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Pred. No. 1.9e-155;
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Factor VIII; blood clotting; haemophilia A;

gene therapy;

vector; human;

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03-JUL-1996;
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P-PSDB; AAW44372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                        and As ractor viii domains: The compared of the in vivo fractor VIII, the SQN deletion does not influence the in vivo pharmacokinetics, but the reduced size of the molecule appears to decrease proteolytic degradation. The invention relates to preparations of replication defective recombinant retrovitus (RV) preparations of replication defective recombinant retrovitus (RV) recombinant RV is capable of infecting human cells, is resistant to degradation by human complement and is capable of inducing to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemophilia A patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence includes a coding region for the B domain deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-743 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 vIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 and A3 Factor VIII domains. When compared to plasmid-derived and A3 Factor VIII domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New replication defective recombinant retroviruses - which express B domain-deleted human factor VIII or human factor IX for the \mbox{\ \ domain-deleted}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of haemophilia
                                                                                                                                                                                                                                                                                                                                                             Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;
                                                                                                                                                                                                                                   426 catgcaaatagagctctccacctgcttctttctgtgccttttgcggattctgctttagtgc 485
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                                                                                                                                                        131 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 190
                             666 cgctaagccaaggccactct@gatgggtctgctaggtcctaccatccaggctgaggttta 725
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96US-0696381.
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100.0%; Pred. No. 1.9e-155;
tive 0; Mismatches 0;
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NJ, Greengard J, Hsu DC, Ib
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AAT03571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT03571 standard; cDNA; 6300 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Factor-VIII; blood clotting; haemophilia A; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor-VIII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 tgtggacctggtaaaagacttgaattcaggcctca 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1988;
A human liver cDNA sequence (AAT03571) in expression vector pCLB89 encodes the Factor-VIII precursor (see AAR86863). The cDNA was subjected to loop-out mutagenesis and used in the construction of subjected to loop-out mutagenesis and esd in the construction of vectors utilised in the transformation of e.g. COS, CHO and C127
                                                                                                                                                                                                     deficiency, esp. haemophilia A
                                                                                                                                                                                                                                    New deletion mutant of factor VIII - useful for treating factor VIII
                                                                                                                                                                                                                                                                                                   P-PSDB; AAR86863
                                                                                                                                                                                                                                                                                                                                                                                    pannekoek H,
                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMO ) IMMUNO AG.
                                                                                                                                                   Example 1; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 490
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                                                                                                                                                                                                                                                                                                                                                                                       Van Leen RW, Van Ooyen AJJ, Verbeet MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0201121.
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64..6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88EP-0110468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= C/note= "the sequence is incomplete since it encodes only amino acids 1-2079 of mature Factor-VIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7..63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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RESULT 14
                                                                                                                                                                                                 Factor VIII; blood clotting disorders; ss.
                                                                                                                                                                                                                                                   Factor VIII cDNA insert of pCLB89
                                                                                                                                                                                                                                                                                                              08-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                AAN81439;
                                                                                                                                                                                                                                                                                                                                                                                        AAN81439 standard; cDNA; 8241 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6300 BP; 2026 A; 1340 C; 1323 G; 1611 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              short peptide (AAR86864), And CR is amino amino acids 1638-2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9aaagagaatggtccaatggcdtctgacccactgtgccttacctactcatatctttctca 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                               /product=factor VIII
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%; Score 575; DB 17; 1
100.0%; Pred. No. 2.1e-155;
tive 0; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 575;
366 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag
                                                                                                                                                                                                   726 tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttccatgctgt 785
                                                                                                                                                                                                                                                                                               666 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725
                                                                                                                                                                                                                                                                           246 cyctaagccaagyccaccotygatggytctyctagytcctaccatccagyctgagyttta
                                                                                                                                                                                                                                                                                                                                                                     186 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 245
                                                                                                                                                                                                                                                                                                                                                                                           606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The cDNA was prepd. from human liver RNA. Clone pCLB89 was produced by combining inserts from several positive clones isolated from the cDNA library. The sequence can be inserted into expression vectors for the prodn. of recombinant factor VIII. The protein produced is useful for treating blood clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 catgcaaatagagctotccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8241 BP; 2625 A; 1759 C; 1703 G; 2154 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; ; 02pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression system for producing factor VIII polypeptide in microbial cells - contg. open reading frame and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiation and termination regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAP81113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 catgeaaatagageteteeacetgettetttetgtgeetttttgegattetgetttagtge 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1987;
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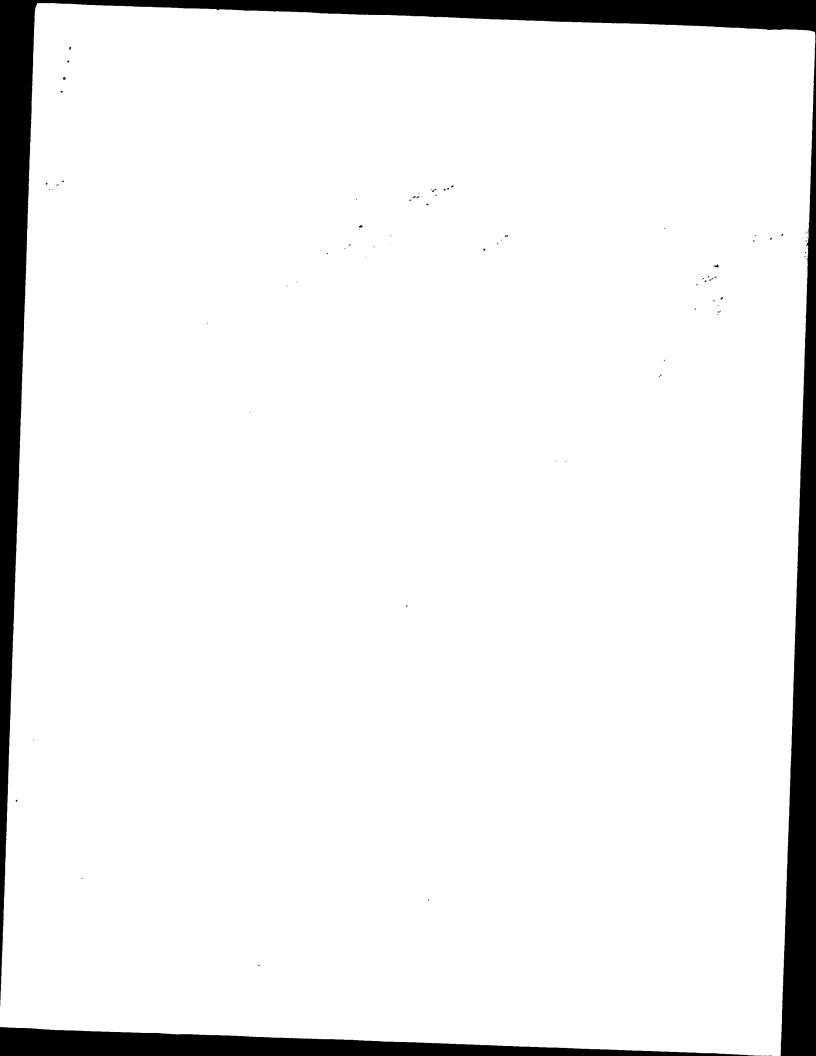
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RESULT 15
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                                                                                                         The isolation of Factor VIII mRNA from human liver, and the preparation, purification and identification of cDNA and its assembly in the plasmid purification and identification of cDNA and its assembly in the plasmid period of the security of the patent preparation of plasmid period of the security of the invention application EP 0253455. The Factor VIII polypetides of the invention application or "B domain" as well as a portion of the 92 kD region has been region or "B domain" as well as a portion of the 92 kD region has been deleted. The polypetides have enhanced factor VIII activity and/or decreased immunogenicity and can be used for the treatment of decreased immunogenicity and can be used for the treatment of the Abs. Haemophilia A. They can also be used to prepare antibodies. The Abs. can be used to determine the concn. of Factor VIII in a body fluid. Sequence 8241 BP; 2625 A: 1759 C; 1703 G; 2154 T; 0 other;
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                                                                                                                                                                                                                                                                                                                          Proteins having Factor VIII activity - comprising deletion mutant proteins of Factor VIII in which central region has been daleted
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426 catgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
                                                       Match 57.5%; Score 575; DB 9; L
Local Similarity 100.0%; Pred. No. 2.4e-155;
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                                            575; Conservative
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88EP-0201209.
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Search completed: January Job time: 12576 sec



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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/bcffUS_COMB.seq:*
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US-07-864-004B-3

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US-08-212-133A-1

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US-08-474-503-1

US-08-670-707A-1

US-09-037-601-1
US-08-121-202-1

US-08-484-891-7

US-08-683-8398-2

US-08-717-294-41

US-08-77-594A-1

US-08-276-594A-1

US-09-324-867-1

US-08-212-133A-7

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Query Match Best Local Similarity 100.0%; Score 1000; DB 4; Length 11933; Best Local Similarity 100.0%; Pred. No. 5.2e-308; Matches 1000; Conservative 0; Mismatches 0; Indels 0; 0  Qy 1 cagctgcgctcgctcgctcactgaggccgggcaaagcccgggcgcggcgcggcgcggcgcggcg	cs for Expression of	28 443 44.3 7493 5 PCT-US94-13200-5 Sequence 29 413.8 41.4 4334 2 US-08-670-707A-38 Sequence 30 413.8 41.4 6402 2 US-08-670-707A-36 Sequence 31 413.8 41.4 6402 2 US-08-670-707A-36 Sequence 32 413.8 41.4 6402 2 US-09-37-601-36 Sequence 34 14.4 14.4 14.4 14.4 14.4 14.4 14.4 1
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                                         CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
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Patent No. 6221349
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SOFTWARE: PatentIn Ver.
SEQ ID NO 13
LENGTH: 11933
                                                                                                                                                                APPLICANT: Couto, Linda B. APPLICANT: Colosi, Peter C. TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS
                                                                                                                                                      FILE REFERENCE: AVIGEN-03743
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901 gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt
                                              781 gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
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APPLICANT: COUTO, Linda B.

APPLICANT: Colosi, Peter C.

ITITLE OF INVENTION: Adeno-ssociated Vectors for Expression of Factor VIII

TITLE OF INVENTION: by Target Cells

FILE REFERENCE: Avigen-04082

CURRENT APPLICATION NUMBER: US/09/470,618

CURRENT FILING DATE: 1999-12-22

EARLIER APPLICATION NUMBER: 09/364,862

EARLIER APPLICATION NUMBER: 60/364,862

EARLIER APPLICATION NUMBER: 60/25,974

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1999-03-24

EARLIER FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0
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US-09-470-618-14
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Patent No. 6200560
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US-09-364-862-14
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CURRENT APPLICATION NUMBER: US/09/364,862

CURRENT FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER FILING DATE: 1999-03-24

EARLIER FILING DATE: 1998-10-20

RARLIER FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic \textsc{US-09-364-862-14}
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                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14
                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Colosi, Peter C.
                                                                                                                           Best Local
                                                                                                                                         Query Match
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                                                                                                              859;
                                                                                                                               Similarity
                                                                                                               Conservative
                                                                                                                               72.5%;
                                                                                                               0; Mismatches 118; Indels 23; Gaps
                                                                                                                               Score 725.2; DB
Pred. No. 1e-220;
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US-08-882-083-1
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                                                                            GENERAL INFORMATION:
      APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       950 teteatgtggacetggtaaaagaettgaatteaggeetea 989
                                                                                                                                                                                                                              961 tctcatgtggacctggtaaaagacttgaattcaggcctca 1000
                                                                                                                                                                                                                                                                                 890 gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710 gtttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcat 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 cggcaggtaagtgccagggaatgtttgttcttaaataccatcgctccagggaatgtttgt 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 aggcaggtaagtgccgtgtgtgggttcccgcggggcctggcctctttacgggttatggccct 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gatctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
782 ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtc
                                                                                                                                722 tttatgatacagtggtcattacactttaagaacattggcttcccatcctgtcagtcttcatg
                                                                                                                                                                          270 ACATCGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCCATCCAGGCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                         662 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 721
                                                                                                                                                                                                                                  210 TCAACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCA
                                                                                                                                                                                                                                                 602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca
                                                                                                                                                                                                                                                                                          482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggaactatatgcaaagtg 541
                                                                                                                                                                                                                                                                                                                                                                                                                          422 ccaccatgcaaatagagctctccacctgcttctttctgtgcgctttttgcgattctgcttta 481
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: US 08/558,107
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  90 GTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                        CTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTC
                                                                                                                 TTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                          CCACCATGGAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTA 89
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35..5017
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(202)672-5399
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SYSTEM: PC-DOS/MS-DOS
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99.8%;
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patent No. 5910481
GENERAL INFORMATION:
                                                                                                                                                                                                                                             US-08-558-107-1
                                                                                                                                                                                                                                                                                              TELEX: 904136
TELEX: 904136
INFORMATION FOR SEO ID NO: 1: .
SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
TYPE: nucleic acid
TYPE: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VOORBERG,
                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,715
REFERENCE, DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                       APPLICATION NUMBER:
                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                            STRANDEDNESS: sin
TOPOLOGY: linear
542 atctcggtgagctgcctgtggacgcaagatttccttcctagagtgccaaaatcttttccat 601
                                              150 ATCTCGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCAT 209
                                                                                                                                                                                              Local
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                                                                                                                                                                                        578;
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                                                                                                                                                                                                  Similarity
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35..5017
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                                                                                                                                                                                                   57.7%;
99.8%;
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 Mismatches

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; NAME/KEY:
; LOCATION:
US-09-243-539-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtc 841
                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 TTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 CTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTC 449
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                              FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P. 13
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 01
APPLICATION NUMBER: 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                              FEATURE:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                  REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                          TELEFAX:
                                                            TOPOLOGY:
                                                                        STRANDEDNESS: single
                                                                                       TYPE:
                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                 20007-5109
                                                                                 nucleic acid
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3000 K Street, N.W., Suite 500
                                                                                                       5035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                              (202)672-5399
                    CDS
35..5017
                                                               linear
                                                                                                                                                                                                                                                                             US 08/558,107
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                                                                                                                                                                                                             30472/212
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Query Match

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PATENT NO. 5171844

APPLICANT: VAN OOYEN, ALBERT J.J.; PANNEKOEK, HANS; VERBEET, MARTINUS P.; VAN LEEN, ROBERT W.

TITLE OF INVENTION: PROTEINS WITH FACTOR VIII ACTIVITY PROCESS FOR THEIR PREPARATION USING GENETICALLY-ENGINEERED CELLS AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               5171844-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                 ; SEQ ID NO:1:
                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                        Matches 575;
                        486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                             426 catgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
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                                                                          . 6 catgoaaatagagetetecaeetgettetttetgtgeettttgegattetgetttagtge 65
       66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         570 CTCATGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 608
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                                                                                                                                                                                                                                                                            LENGTH: 8241
                                                                                                                                                                                                                                                                                                          FILING DATE: 10-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 TCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACCTTACCTATATCTTT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 CTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTC 449
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                                                                                                                                                                                   Similarity
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                                                                                                                                                     57.5%; Score 575; DB 6; L6
100.0%; Pred. No. 9.2e-173;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.78; Score 577.4; DB 3; Length 5035; 99.88; Pred. No. 1.2e-173; Indels 0;
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                                                                                                                                                                                     Length 8241;
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                          TELEFAX: (619) 452-2616
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 base pairs
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GENERAL INFORMATION:
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                                                                                           REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 930049.438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 452-1288
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,851A
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            STREET: 110.
STREET: San Diego
CTATE: California
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                  TYPE:
STRANDEDNESS:
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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STREET: 11055 Roselle
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             nucleic acid
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SYSTEM: PC-DOS/MS-DOS
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Chang, Steven
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US-08-366-851A-1
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US-07-864-004B-3
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                                                                                                                                Sequence 3, Application US/07864004B patent No. 5364771
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    169
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                                                                                                                                                                                                                                                                                                                                                   Match 57.5%; Score 575; DB 1; Local Similarity 100.0%; pred. No. 9.6e-173; Local S75; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                         906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
                                                                                                                                                                                                                                                  966 tgtggacctggtaaaagacttgaattcaggcctca 1000
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  649 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 683
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 228
                                                         STREET: 1100 I
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                         COUNTRY:
                                                                          ADDRESSEE:
                                                                                                                          INFORMATION:
                                  30309
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110..7165
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                                                  Georgia
                                                                 E: Kilpatrick & Cody
1100 Peachtree Street
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US-07-864-004B-3
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: EMTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              426 catgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE:
                                                                                                                                                                                                                                                                                                 486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                    150 CATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTCCGATTCTGCTTTAGTGC 209
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                                                                                                                                                                                                                                       210 CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 269
                                                                                                                                                                                                     606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                            666 ogctaagccaaggccaccotggatgggtctgctaggtcctaccatccaggctgaggttta 725
                                                                                                                                                                                         330 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACAT 389
                                                                                                                                          390 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 449
510 TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG
                                                           786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9009 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                    57.3%; Score 573.4; DB 1; Length 9009; 99.8%; Pred. No. 3.1e-172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Equivalent to the A3-C1-C2
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                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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US-08-251-937A-3
    Best Local Similarity
                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           MOLECULE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08251937A Patent No. 5583209
                                                                                                                                                 OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                    OTHER INFORMATION: /note= "Equivalent to the Al-A2 OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 404-815-6367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/04/251,937A
FILING DATE: 31-MAY-1994
                                                                                                   NAME/KEY: misc_feature (Domain Structure)
LOCATION: 1 2277
                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                               NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5001 . . . 7053
                                                                                                                                                                                                                                  TISSUE TYPE: Liver
                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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7: US
                                                                                                                                                                                                                                                                                                                                                                              9009 base pairs
                                                                                                                                                                                                                                             Homo sapien
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1100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                          linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                             NO
O
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                                                                                                                                                                                                                                                                                                                                                      single
    57.3%;
99.8%;
                                                                                                                                                 /note= "Equivalent to the A3-C1-C2 domain"
Pred. No. 3.1e-172;
             Score 573.4; DB 1;
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        Length 9009;
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RESULT 12
US-08-212-133A-1
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Patent No. 5663060
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      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЪ
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              APPLICANT: Lollar, John S. APPLICANT: Runge, Marschall S. TITLE OF INVENTION: Hybrid Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 574; Conservative
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                             APPLICATION NUMBER: US/08/212,133A FILING DATE: March 11, 1994
                                                                                                                                                                                                                                         STREET: 100 P
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    690 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30303
Pabst, Patrea L.
                                                                                                                                                                                                                    Georgia
f: US
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                                                                                                                                                                                                                                                         100 Peachtree Street
                                                                                                                                                                                                                                                                     Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                       Hybrid Human/Animal Factor VIII
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REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMI

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US-08-212-133A-1
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Best Local Similarity 99.8%;
Matches 574; Conservative
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INFORMATION FOR SEQ ID NO: 1:
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TELEPHONE: 404-572-5508
TELEFAX: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9009 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5125 7053
OTHER INFORMATION: /note= "Equivalent to
                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..2277
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
                                                                                                                                                                                                              606 cacctcagtcgtgtacamaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                    330 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACAT 389
                                                                                                                     390 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 449
                                                                                        786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
                                                                                                                                                                                    666
cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "cDNA encoding human factor VIII."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Equivalent to the A3-C1-C2
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Equivalent to the Al-A2 domain."

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                 Score 573.4; DB 1; Length 9009; pred. No. 3.1e-172;
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; Sequence 1, Application US/08474503 ; Patent No. 5744446
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                                                                                                                US-08-474-503-1
 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.3%;
Best Local Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                   Matches 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: pratt, John S.
REGISTRATION NUMBER: 29,476
REFERENCE/DOCKET NUMBER: EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6500
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pair
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                      LOCATION: 1..2277
OTHER INFORMATION:
OTHER INFORMATION:
-474-502-1
                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature (Domain Structure) LOCATION: 5125 . 7053
                                                                                                                                                                                                                                                                                                         TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                        NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 ... 2277
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                                                                                                                                                                                                                                                                                                                                                                                                                             9009 base pairs
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                                                       Conservative
                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                  /note= "cDNA encoding human factor VIII."
                                                                                                                                                                                                                                               /note= "Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                                                /note= "Equivalent to the Al-A2 domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMU106CIP(3)
                                                          0; Mismatches
                                                                     Score 573.4; DB 1; Length 9009; pred. No. 3.1e-172;
                                                                     Gaps
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                                                                APPLICATION NUMBER: W0 PCT
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08670707A Patent No. 5859204 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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              FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin-Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                      PRIOR APPLICATION DATA: ":
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Greenlee, Wloner and Sullivan, P.C.
                          APPLICATION NUMBER: US 0: FTLING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lollar, John S. TITLE OF INVENTION: Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                              APPLICATION NUMBER: US/08/670,707A FILING DATE: 26-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
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Greenlee, Lorance L.
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                                      US 07/864,004
                                                                              US 08/212,133
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906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca
                                           510 TEGTGTATCCTACTEGAAACCTTCTGAGGGGAGCTGAATATGATGATGACCAGTCAAAG 569
                                                                                                              786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION: /note= "Equivalent to the A3
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OTHER INFORMATION: /note= "cDNA encoding human factorVIII"
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REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: not
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 Mismatches

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Pred. No. 3.1e-172;
0; Mismatches 1; Indels 0;
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TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE: 26-JUN-1
CLASSIFICATION:
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ferber, Donna M. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/864,004 FILING DATE: 07-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO POFILING DATE: 15-NOV-1994
                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 5125..7053 OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                   OTHER INFORMATION: /product= "Domain Structure" OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                 NAME/KEY: misc_feature
LOCATION: 1.2277
OTHER INFORMATION: /product= "Domain Structure"
OTHER INFORMATION: /note= "Equivalent to the A1-A2 domain"
                                                                                                                                                                                                                                        TISSUE TYPE:
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              NAME/KEY: misc_feature LOCATION: 1..2277
OTHER INFORMATION: /product= "Domain"
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5370 Manhattan Circle Suite 201
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26-JUN-1996
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, OTHER INFORMATION: /note= "cDNA encoding human factorVIII" US-09-037-601-1
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                                                                                                 966 tgtggacctggtaaaagacttgaattcaggcctca 1000
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                                        gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
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TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
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Search completed: January 8, 2002, 17:19:07 Job time: 12198 sec

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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A1526753 uj42e03 y

BG92386 60284575

BG927142 602846744

BE912296 601666013

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F152291 uz31d07	434 fl32g05.	1428548 fr85e10.	28904 53db Human	532535 6020/458	E348439 DW1/1102.	86//M	F604025 269694	E3/1524 6U12232	10//19 6018928	8/3581 Onbeals	286923 6010926	9/6890 6028456	265337 UKUINUO	172588 6023370	916015 6016663	5686/2 60258/6	136574 6017796	283339 POTTOS	144018 6017912	. ~	383789 6020447	975622 6028453	285283 6010982	914512 6028132	E914540 6016656	1195667 ui52c06	E308999 6010970	138391 601/8254	F14466	653260 AV653260	6259

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                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 954)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG477974 954 bp mRNA EST 21-MAR-2001 602522966F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4641352 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG477974.1 GI:13410253
                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1408 row: c column: 17
                                                                                                                                                               High quality sequence stop: 626.
Location/Qualifiers
                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4641352"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                               AA817854 456 bp mRNA UI-R-AO-ae-g-10-0-UI.S1 UI-R-AO Rattus norvegicus cDNA clone UI-R-AO-ae-g-10-0-UI 3′ similar to gb|L33869|RATCERU Rat norvegicus
          Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                           On Mar 9, 1998 this sequence version replaced gi:2946779
                                                                                                  discovery Genome Res. 6 (9), 791-806 (1996)
University of ·Iowa
                                                                                                                                                               Normalization and subtraction: two approaches
                                                                                                                                                                                              Bonaldo, M.F.,
                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                  Norway rat.
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                                                                                                                                                                                            Lennon, G. and Soares, M.B.
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Pred. No. 2.7e-82;
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similar to
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BF150467
                                                                                                   BF150467
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Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Ovary library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LDNL (info@image.lln1.gov). IMAGE ID=1767329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_2: Eco RI; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, bra. liver, kidney, heart, spleen, ovary, and muscle: The tis a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification the library of origin of a clone within the mixture."

a 105 c 101 g 144 t
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/clone_lib="UI-R-A0"
/dev_stage="adult"
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/db_xref="taxon:10116"
                                       NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666421 5' SW:CERU_MOUSE Q61147 CERULOPLASMIN PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ∕organism="Rattus norvegicus"
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54.8%;
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979 aaagacttgaattcaggcctca 1000
                                              508
                                                                                                                                                                                                                     391 ACCAAGGAGTATGAGGGÄGCCGTCTACCCTGACAACACCACTGATTNTCAACGGGCTGAT 450
                                                                                                                                                                                                                                                                                                              331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                            CCTGGAGAGGGAGACAGCAATTGTGTGACCAGGATNTACCACTCCCATGTTGATGCTCNC 567
                                                                      ccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggta 978
                                                                                                                                                                         gataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggt 918
                                                                                                                                                                                                                                                 GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC 390
                                                                                                                                                                                                                                                                                                                                                                                                                             ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                   GACAAAGTGCTTCCCGGACAACAGTATGTGTGTATGTGCTGCATGCC---AATGAGCCAAGT 507
                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 669)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57/B6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:3666421"
/clone_lib="NCI_CGAP_Mam5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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Pred. No. 2.4e-16;
0; Mismatches 172;
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137 CCAGCCTGGCTTAGGGCTTTTAGGCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 196
                      679 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                   619 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 678
                                                                                           TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                       208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA461838 477 bp mRNA EST 10-UUN-1997
vf95d04.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:851527 5' similar to gb:M13699 CERULOPLASMIN PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
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                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                     adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                      Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_mammary_gland_NbMMG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI526753 625 bp mRNA EST 18-MAR-1942603.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922620 5' similar to gb:M13699 CERULOPLASMIN PRECUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium finfo@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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314 286 1810
/note="organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). xhoI shoul be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                           /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                   /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                /db_xfef="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                /strain*"C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC
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                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10912 row: j column: 22
                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 658)
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                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                /strain="FVB/N"
                                                                        Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602846744F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4977442 5',
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                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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LLAM10972 row: g column: 11
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Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
131 c . .148 g 177 t
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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/note="Torgan: mammary; vector: pcmv-sport6; sality: pcm-sality: pcm-sality
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                                                                                                                                                                                      ORGANISM
                                                             JOURNAL
                                                                                 TITLE
                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 ACCAAGGAGTATGAGGGAGCCGTCTACCCTGACAACACCACTGATTTTCAACGGGCTGAT 495
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                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                           601666013F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3966051 5',
                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                     BE912296
                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 878)
                                                                                                                                                                                                                                                  BE912296.1 GI:10409387
                                                                                                                                                                                                                                                                                           mRNA sequence.
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                            house mouse
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                        cgapbs-r@mail.nih.gov
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161 c 176 g 210 t
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/strain="FVB/N"
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Pred. No. 2.9e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                     CAP trapper.
Mus musculus (Strain C57BL/6J) adult male testis cDNA to mRNA,
Clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                              AK014835 3739 bp mRNA HTC 05-JUL-2001 Mus musculus adult male testis cDNA, RIKEN full-length enriched
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                             clone:4921507J22.
                                                                                                                                                                                AK014835.1 GI:12652907
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                         library, clone:4921507J22, full insert sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://image.llnl.gov
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Clone distribution: MGC clone distribution information can be
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a 188 c 195 g 227 t
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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54.5%;
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Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sakai, K., Saki, D., Shibata, Y., Shibata, Y
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Nature 409, 685-690 (2001)

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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, Adachi, J., Aizawa, K., Akahira, S., Fukunishi, Y., Furuno, M., Adachi, J., Aizawa, K., Pukuda, S., Fukunishi, Y., Furuno, M., Adachi, J., Barana, J., Barana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                                                                              WashIngton Uniwersity School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI225600 1006 bp mRNA EST 29-OCT-1998 uj06c05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1891112 5' similar to gb:M13699 CERULOPLASMIN PRECURSOR
  This clone is available
                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1006)
                                                                                                                                                                                                                                                                                                                                                                                      house mouse. **
                                                                                                                                                Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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                      mouseest@watson.wustl.edu
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/tissue_type="testis"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
/dev_stage="adult" 995 t l others
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/db_xref="MGD:MGI:88476"
/clone="4921507J22"
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Pred. No. 5e-16;
""amatches 171;
royalty-free through
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                                                                                                                                                                                                                                                                                                          CCTGGAGAGGGAGACAGCANTTGTGTGACCAGGATTTACCACTCCCATGTTGATGCTCCA
                                                                                                                                                                                                                                                                                                                               ccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggta
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sequence.
AA865338
AA865338.1
EST.
                                                                            AA865338 521 bp mRNA EST 29-APR-1998 og88d10.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455379 similar to gb:M13699 CERULOPLASMIN PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 463
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3'
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Pred. No. 4.1e-16;
0; Mismatches 172;
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          977 taaaagacttgaattcaggcctca 1000
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                                                                                    gtccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctgg
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                                                 GTCCTGGGGAAGGAGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC 66
                                                                                                                                                                                                                                                                                        ATGACAAAGTATATCCAGGAGAGCAGTATACATACATGTTGCCTTGCCACTGAAGAACAAA 126
                                                                                                                                                                                                             ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG
                                                                                                                                                                                                                                               Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 521)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: -40m13 fwd. ET from Amersham
h quality sequence stop: 360.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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82.33; Pred. No. 5.7e-16;
tive 0; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                   737
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  977 taaaagacttgaattcaggcctca 1000
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                                                                                                                                                                                                                                                                                                                                                                                       ggccaccetggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 736
                                                                                                                                                                                                                                                                            AACCGGTCTGGCTTTTTTAGGCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 318
                                                                     gtccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctgg 976
                                                                                                                                     atgataaagtottoootggtggaagcoatacatatgtotggcaggtootgaaagagaatg 916
                                                                                                                                                                                                                           tcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgtttggtgtatcct 796
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AL556703 LTI_NFL006_PL
prime, mRNA sequence.
AL556703
                                      GTCCTGGGGAAGGAGATGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC 558
                                                                                                                  ATGACAAAGTATATCCAGGAGAGCAGTATACATACATGTTGCCTTGCCACTGAAGAACAAA 498
                                                                                                                                                                                                ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG
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Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://fulllength.invitrogen.com"
169 c 192 g 253 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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52.3%;
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859 gataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggt 918
                                                                                                                                                                                                                   270 CCAGCCTGGCTAGGGTTTTTAGGCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 329
                                                                                                                                                                                                                                                                                                                               619 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                       210 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTCAGACTATAGACAAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                             ACCAAGGAGTATGAGGGAGCCGTCTACCCTGACAACACCACTGATTTTCAACGGGCTGAT 449
                                                                          GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC 389
                                                                                                                                                             attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctac 798
                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.go\psi/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library."
185 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert 2.5 kb. Library constructed by Life Technologias, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-Ii (1996). Note: this is a NCI_CGAP Tibrary "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:4917258"
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/lab_host="DH108"
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Pred. No. 7.9e-16;
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383 ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG
                        617 tytacaaaaaqactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaa 676
                                                                                                                                                                         677 ggccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 736
                                                                                                                                                                                                                                203 TATATAAGAAGGCCCTTTATCTTCAGTACACAGATGAAACCTTTAGGACAACTATAGAAA 262
                                                                                                                                                                                                                                                                                                                                   Match 9.0%;
Local Similarity 52.1%;
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                                                                                                             tcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcct 796
                                                                                                                                                     AACCGGTCTGGCTTGGGTTTTTAGGCCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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351 Guo Shoujing Road, Zhangjiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
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xhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GLCDJA09"
/clone_lib="GLC"
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/db_xref="taxon:9606"
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Pred. No. 1.8e-15;
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Zhangjiang Hi-Tech Park, Pudong, Shanghai
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                         739 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgttatcctac 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/clone="IMAGE:4022022"
/clone_lib="NGI_CGAP_LU30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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574 c 580 g 572 t
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/db_xref="taxon:32630"
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TITLE
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AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1040
                     agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                  cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
                                                                          CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 1100
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University, 190 Frelinghuysen Road, Piscataway, NJ 0885
Sequence update by submitter
On Oct 3, 2000 this sequence version replaced gi:209216
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-APR-1993) Waksman Institute, Rutgers
Submitted (27-APR-1993) Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning vector pucks
artificial sequence; vectors.
1 (bases 1 to 2368)
Vieira,J. and Messing,J.
New pUC-derived cloning vectors with different selectable markers
and DNA replication origins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University, 190 Frelinghuysen Road, Piscataway, (bases 1 to 2368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-SEP-2000) Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vieira,J.
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                          /transl_table=11
/product="beta-lactamase"
/product="beta-lactamase"
/product="beta-lactamase"
/protein_id="Aaci8332.1"
/protein_id="Aaci8332.1"
/db_xref="GI:10504975"
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/translation="MSIOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
/translation="MSIOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
/TELDLNSGKILLESFRPEERFPMMSTFKVLLCGAVLSRIDAGOEQLGRRIFYSONDLYE
YSPVTEKHLTDGMTVRELCSAAITMSONTAANLLLTTIGGFRELTAFLHWEDHVYRE
YSPVTEKHLTDGMTVRELCSAAITMSONTAANLLLTGELLTLASRQOLIDWHEADKVAGPL
DRWEPELNEAIPNDERDTTMFVAMATTLRKLLTGELLTLASRQOLIDWHEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                        EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Cloning vector pUC6S"/db_xref="taxon:137702"/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA 620
                                                                                                                                                                                                                                                                                                                                                         CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT 440
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                                                                                                                                                                                                              tttcgtctcgcgcgttetcggtgatgacggtgaaaacctctgacacatgcagctcccggag 900
                                                                                                                                                                                                                                                                                                                           gtctaagaaaccattattatçatgacattaacctataaaaataggcgtatcacgaggccc 840
                                                                                                                                                                                                                                                                                                                                                                                atttagaaaaataaacaaataggggttdcgcgcacatttccccgaaaagttgccacctgac
                                                                                                                                                                              TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                                                                                 GCGGGTGTTGGCGGGTGTCGGGGCTTAACTATGCGGC 159
                                                                                Cloning vector pSP70.
x65330
                       promoter.
Cloning vector pSP70.
Cloning vector pSP70
                                                                                                        CVPSP70
artificial sequence;
1 (bases 1 to 2417)
                                                        beta-lactamase; bla gene;
                                                                     x65330.1 GI:58235
                                                                                                   2417 bp
              vectors
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                                                           cloning vector; multiple cloning site;
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                                                                                                                                                                                                                                                                                                                 1364 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1423
                                                                                                                                                           1424
      1544
                                                                                                                                                                                                 121
61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                           tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                         CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1483
                                                                                                                                                                              cgctcgtcgtttggtatggcttcattcagctccggttccccaacgatcaaggcgagttaca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technical, Services.

Direct Submission
Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-MAY-1993) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA 368 x65300-X65335 for related vector sequences This vector can be obtained from Promega Corporation, Madison, William Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Technical, Services.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Order or Technical 800-356-9526
In Wisconsin 800-356-9526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  revised by 2]
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Beta-lactamase"
/product="Gena6430.1"
/protein_id="GAA6430.1"
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/translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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/TELDLNGGKILESGREPERFPMMSTFKVLLCGAVLERGADGQEQLGARTHYSONDLVE
TELDLNGGKILTDGMTVRELCSAAITMSDNTAANLLLTTIGELLTLASRQOLIDMMEADKVAGPL
DRWEPELNEAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
RSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1090. .1950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SP6 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Cloning vector psp70"
/db_xref="taxon:90135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="multiple cloning sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="T7 promoter'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="T7 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2401. .2417
/note="SP6 promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         599 c
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1001; DB 12; Length 2417; 100.0%; Pred. No. 1.2e-274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   608-274-4330
                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1844 TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1724 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9c999t9tt9gc999tgtc9g9gctg9cttaactatgc99c 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCCGTCAGGGCGCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atttagaaaaataaacaaataggggttccgcgcacatttcccccgaaaagtgccacctgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGGGGGATACATATTTGAATGT 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caatattattgaagcatttatcagggttattgtctčatgagcggatacatatttgaatgt 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
Submitted (28-MAY-1993) Technical Services, Promega 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA See X65300-X65335 for related vector sequences
                                                                                                           Direct Submission
Submitted (23-MAR-1992) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                          artificial sequence; vectors 1 (bases 1 to 2419)
Technical, Services.
                                                                                             revised by [2]
2 (bases 1 to 2419)
                                                                                                                                                                                                                                    Cloning vector psp71
                                                                                                                                                                                                                                                                         beta-lactamase; bla gene; cloning vector; multiple cloning
                                                                                                                                                                                                                                                                                                                                     Cloning vector pSP71
                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
                                                            1666 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
                                                                                                                                                                                                                                                 1546
                                                                                                                                                              1606
421 ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
                                                                                361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                          1486 TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1545
                                                                                                                                                                                                                                                                                                                                                                                            1426 CGCTCGTTGGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCCAACGATCAAGGCGAGTTACA 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1366 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga 360
                                                                                                                                                                                                                                                   241 agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
                                                                                                                                                                                                                                                                                                                                  181 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                                                                                                                                    121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
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                                                                                                                                             GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA 1665
                                                                                                                                                                                                                             AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This vector can be obtained from Promega Corporation, Madison, WI Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Order or Technical 800-356-9526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Beta-lactamase"
/product="Beta-lactamase"
/product="Gercaha6431.1"
/protein_id="CAA46431.1"
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IELDLNSGKILESFRPEERFPMMSTFKVLLGGAVLSRIDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIFNDERDTTMPVAMATTLRKLLTGELLTLASRQQLLDWMEADKVAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2402. .2419
/note="SP6 promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="T7 transcription initiation site" complement(1092. .1952) /gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1092. .1952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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/db_xref="taxon:90136"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1001; DB 12; Length 2419; 100.0%; Pred. No. 1.2e-274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608-274-4330
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1 (bases 1 to 2450)
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                                                                                                                                                                                                                                                                                                                                                                                            U74374.1 GI:1649038
                                                                                                                                                                                                        Submitted (11-OCT-1996) Stanford University, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                   2 (bases 1 to 2450)
Fan,J.-B., Quackenbush,J. and Myers,R.M.
Direct Submission
                                                                                                                                                                                                                                                                                                      Fan, J.-B., Quackenbush, J. and Myers, R.M.
                                                                                                                                                  855 California Ave.
Palo Alto, CA 94304 USA.
                                                                                                                                                                             Stanford Human Genome Center
                                                                                                                                                                                              Contact: R. M. Myers
                                                                                                                                                                                                                                                                                           pJF5 Cloning Vector
                                                                                                                                    Ampicillin Resistance Selectable Vector used
                                                                                                                                                                                                                                                                             Unpublished (1996)
/note="Multiple Cloning Site
XhoI/PvuII/BstXI/XbaI/BamHI/EcoRI/BstXI/EcoRV/BglII"
                                     /note="SP6 transcription initiation site"
                                                                              organism="Cloning Vector pJF5"
                                                                   /db_xref="taxon:53561"
                                                                                                            ocation/Qualifiers
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                                                                               gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                          TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAAGGCAAAAT
                                                                                                                                       tetteageatettttaettteaecagegtttetgggtgageaaaaacaggaaggeaaaa 600
                                                                   GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTTTT 1996
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YSÞVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTTGGPKBLTAFLHNMGDHVTRL
DRWEÞELNEAIFNDERDTTMÞVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGÞL
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ETGASLIKHW"
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/product="beta-lactamase"
/protein_id="AAB17670.1"
/protein_id="AAB17670.1"
/db_xref="G1:1649039"
/translation="MSIQHERVALIPEFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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/note="SP6 promoter"
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                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JAN-2000) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, W1 53711-5399, USA on Jan 26, 2000 this sequence version replaced gi:58239. See X65300-X65335 for related vector sequences
                                                                                                                                                                                                                                                                                Outside U.S.
                                                                                                                                                                                                                                                                                          Order or Technical 800-356-9526
In Wisconsin 800-356-9526
                                                                                                                                                                                                                                                                                                                                    This vector can be obtained from Promega Corporation, Madison, Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           revised by [3]
3 (bases 1 to 2462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Cloning vector pSP72.
Cloning vector pSP72
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                        complement(1135. .1995)
/gene="bla"
complement(1135. .1995)
                                                                                                                      /note="multiple cloning sites"
99. .118
                                                   /note="T7 transcription initiation site"
                                                                                                                                                              /note="SP6 transcription initiation site"
                                                                                             /note="T7 promoter"
                                                                                                                                                                                                      /organism="Cloning vector psp72"
/db_xref="taxon:90137"
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s Hollow Road, Madison, Wi 53711-5399, USA
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                                                                                                                                    1949 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTCCTTTTT
                                                                                  2009
                721 atttagaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780
                                                                                                                                                                                                                                                                     1829 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA 1888
                                                                                                                                                                                                                                                                                                                                       1769 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                         1709 GAATAGTGTATGCGGCGACCGACTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
                                                                                    661 caatattattgaagcatttatcagggttattgtctcatgagcgggatacatatttgaatgt 720
                                                                                                                                                                                                                    541 tottcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaat 600
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                                                                                                                                                                                                                                                                                       481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccaactcgtgcacccaactga 540
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                                                                                                                                                                                                                                                                                                                                                                                                                         361 gaatagtgtatgcggcgaccgagttgctcttgcccgggcgtcaatacggggataataccgcg 420
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                                                                  CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT
                                                                                                                                                      9ccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                                                                                                    TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA 1708
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/note=14 c 605 g
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/protein_id="CAA46432.1"
/db_xref="GI:58240"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2309 GCGGGTGTTGGCGGGTGTCGGGGCTTAACTATGCGGC 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JAN-2000) Technical Services, promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA on Jan 26, 2000 this sequence version replaced gi:58241. See x65300-x65335 for related vector sequences see x65300-x65335 for related vector sequences the sequences of the sequence of the sequences of the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-MAY-1993), Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA revised by [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequence; vectors.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Order or Technical 800-356-9526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Call one of the following numbers for order or technical
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                                                                                                                                                                                                                                                                                                                                   /note="SP6 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:90138"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Cloning vector psp73"
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                                                                                                                                                                                /note="T7 transcription initiation site"
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/product="Beta-lactamase"
                                                           /c6don_start=1
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1471 CGCTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1530
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361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
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                                                                             2071 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGGAAAAGTGCCACCTGAC
                                                                                                                                                      2011 CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT 2070
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                                                                                               721 atttagaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac
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/db_xref="GI:58242"
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1459 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1518
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                    61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
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                                                                                    1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-NOV-1997) Philippsen P., Applied Microbiology, University of Basel, Biozentrum, Klingelbergstr. 70, Basel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wach,A., Brachat,A., Pohlmann,R. and Philippsen,P. New heterologous modules for classical or PCR-based gene disruptions in Saccharomyces cerevisiae Yeast 10 (13), 1793-1808 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philippsen, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASAJ2679 2512 bp DNA SYN 28-MAR-2000
Synthetic DNA containing Escherichia coli plasmid pEA6a, bla gene,
multiple cloning site, pSP72 derivative.
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1 (bases 1 to 2512)
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beta-lactamase; bla gene.
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                                                                                                                                                                                                                                                                                             DRWEPELNEAIPNÖERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
                                                                                                                                                                                                                                                                                                           /translation="MSIQHFRVALIPFFAAFGLPVFAHPETLVKVKDAEDOLGARVGY IELDLNSGKILESFRÞEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE YSPYTEKHLTDGMTVRELCSAAITMSDMTAANLLLTTIGGFKELTAFLHNMGDHYTRL
                                                                                                                                                                                                                                                                          LRSALPAGWEIADK$GAGERG$RGIIAALGPDGKP$RIVVIYTTG$QATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                          /product="beta-lactamase"
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/db_xref="GI:2623974"
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/transl_table=11 ,
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/gene="bla"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Multiple cloning site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga
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                                 Synthetic construct synthetic construct
artificial sequence.
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                                                                                                            PUC8 cloning vector
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COMMENT
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                 Query Match 100.0% Score 1001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsvier 1985 and supplements
#comment vector I-A-iv-20
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#journal Gene (1982) 19: 259-268
#comment. see also 'note added in proof'
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268- 426 1303-1461
427- 526 2351-2252
527- 663 2210-2074
                                                                                                                                                                                                                                                                                                                                pUC8 source
mut 1107 T C 3912
mut 1408 A G 361
                                                                                                                                                                                                                                                                                                                                                                                        664-2665 4355-2354 (c) pBR322 Conflict (cfl) and Mutations (mut):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Features of pUC8 (2665 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #offspring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #complement
                                                                                                                                                                                                   #indicator beta-galactosidase
MARY pUC8 #length 2665
                                                                                                                                                                                                                                                                                               931-1719 1-789 Ap-R; b-lactamase
                                                                                                                                                                                                                                          #resistance Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VecBase(3):pUC81, VecBase(3):pUC82, VecBase(3):pIC7 PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VecBase(3):pUC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VecBase(3):pUC7, VecBase(3):M13mp8, VecSource(3):bGal8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VecBase(3):pUC8c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residue
 Conservative
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                                                                                                            /organism="synthetic construct
/db_xref="taxon:32630"
680 c 670 g 661 t
                                                                                                                                                                 1. .2665
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         2210-2074
4355-2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
6002-6427
1069-1297
1- 36
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                                                                                                                                                                                                                                                                                                                                (c) pBR322
(c) pBR322
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(c) pBR322
(c) pBR322
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #TYPE DNA CIRCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lac-Operon polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M13mp8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lac-Operon
                                                                                                                                                                                                           #checksum
                         1.2e-274;
                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of M13mp8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m, VecBase(3):pEMBL8p, VecBase(3):pOM4,
         Indels
                                          Length 2665;
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           Gaps
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                                    RESULT
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1330 TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                  421 ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
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                                                                                                                                                                                                                                                                                                                                                                     910
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                                                                                                                                                                                                                                                                   850 CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
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                                                                                                                                                                                                                                                                                                                                                                    GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTTTT
                                                                       GCGGGTGTTGGCGGGTGTCGGGGCTTGGCTTAACTATGCGGC
                                                                                                                                  acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                                                                                                                                                                                                     GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                                                                                                                gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
                                                                                   gcgggtgttggcgggtgtcggggctggcttaactatgcggc 1001
                                                                                                                     ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA
                                                                                                                                                                     TTTCGTCTCGCGCGTTTCCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCCGGAG
pUC9 cloning vector
           SYNPUC9V
            2665 bp
               DNA
                circular
                SYN
                  26-JUL-1993
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COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
         SUMMARY
                                                                 SELECTION
                                                                         POLYLINKER HindIII-PstI-SalI-BamHI-SmaI-EcoRJ
                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                        PARENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               These data and their annotation were supplied to GenBank by Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLECTION ATCC 37252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION VB0022
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1 (bases 1 to 2665)
                                                                                                                              pUC9 source
mut 1107 T C 3912 (c) pBR322
mut 1408 A G 3611 (c) pBR322
                   #resistance Ap*
#indicator Meta-galactosidase
                                                                                             931-1719 1-789 Ap-R; b-lactamase
                                                                                                                                                                                                Conflict
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                                                                                                                                                                                                                527 - 663
664 - 2665
                                                                                                                                                                                                                                                                                                                                                              Features of pUC9 (2665 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembled from pUC19 and M13mp9 by F. Pfeiffer, MPI, Martinsried Revised 16-DEC-1986 by F. Pfeiffer:
2287/8 'AT' to 'TA' to match revised sequence of PBR322
The strand shown contains the beta-galactosidase mRNA sequence including the multiple cloning site of M13mp9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #offspring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #parent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Pouwels P.A., Enger-Valk B.E., Branmar W.J. #book Cloning Vectors, Elsvier 1985 and supplements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #Comment vector I-A-iv-20
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1- 426
1- 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Vieira J., Messing J.
#journal Gene (1982) 19: 259-268
#comment see also 'note added in proof'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence
                                                                                                                                                                                                                                                                                                                                                                                              VecBase(3):pUC91, VecBase(3):pUC92
VecBase(3):pIC19R
VecBase(3):pICEM19Hm, VecBase(3):pICEM19Hp,
VecBase(3):pICEM19Rm, VecBase(3):pICEM19Rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VecBase(3):pUCl3, VecBase(3):pEMBL9m, VecBase(3):pEMBL9p, VecBase(3):pUC931, VecBase(3):pOM1, VecBase(3):pOM3,
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     puc9
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2351-2252 (c) F
2210-2074 (c) F
4355-2354 (c) F
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6372-6797
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 #length 2665
                                                                                                                                                                                                                               рвк322
рвк322
                                                                                                                                                                                                              pBR322
                                                                                                                                                                                                                                                                   polylinker of M13mp9
Lac-Operon
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901 acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                           670 TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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                                                                 841 tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag 900
                                                                                                                             730 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                                                                                              790 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGGAAAAGTGCCACCTGAC
                                                                                                                                                                                                                                 721 atttagaaaaataaacaaataggggttccgcgcacatttcccccgaaaagtgccacctgac 780
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                                                                                                                                                   781 gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 840
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                                                                                                                                                                                                                                                                                                                                                                                  910 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTCCTTTTT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1270 AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1450 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1391
                                                                                                                                                                                                                                                                                                                                                                                                        601 gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactctttccttttt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaat 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1510 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtccttccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; Score 1001; DB 12; Similarity 100.0%; Pred. No. 1.2e-274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:32630"
679 c 671 g
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1. .2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961 gcgggtgttggcgggtgtcgggcttggcttaactatgcggc 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 GCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGC 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE pIC7 - Cloning vector DATE 25-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. pIC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obtained from VecBase 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artificial sequence.
1 (bases 1 to 2668)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic construct DNA.
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#journal Gene (1984) 32: 481-485
#title
                                                                                                                                                                                                                       To produce greater versatility of insertional inactivation of beta-galactosidase activity for subcloning and sequencing, a chemically synthesized oligonucleotide, specifying nine restriction sites including BglII, XhoI, NruI, ClaI, SacI and EcorV in various configurations with existing polylinkers, was created. These improved polylinkers were inserted into plasmids for routine cloning of ds-DNA and into chimeric phage/plasmids for biological production of ss-DNA. The most versatile polyrecognition pattern specifies 17 restriction sites in the beta-galactosidase alpha-complementing gene fragment. Clone pIC7 was used to produce all the other polylinker-carrying vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembled from pUC8 and GenBank:pIC7 by F. Pfeiffer COMMENT For construction of pTC7, a synthetic oligonucleotide has been used to replace the pUC8 polylinker and thus to construct a new cloning vector with a different polylinker. The other pIC-vectors are based on this new pIC7 polylinker, which was combined with the existing pUC9 and pUC19 polylinkers in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pIC19R: EcoRI- Poly (pIC7) -HindIII- Poly (pUC9) -EcoRI pIC19H: HindIII- Poly (pUC9) -EcoRI - Poly (pIC7) -HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pIC20R: ECORI- POly (PIC7) -HindIII- POly(PUC19) -ECORI PIC20H: HindIII- POly(PUC19) -ECORI - POly (PIC7) -HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pIC19 and pICEM19 vectors:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     following arrangements:
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                                                                                                                                #parent
                                                                               #offspring
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VecBase(3):pIC19H, VecBase(3):pIC19R,
VecBase(3):pIC20H, VecBase(3):pIC20R,
VecBase(3):pICEM19Hm, VecBase(3):pICEM19Hp,
                                                                                                  VecBase(3):pUC8, GenBank(50):pIC7
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661 caatattattgaagcatttatcagggttattgtctcatgaagcggatacatatttgaatgt 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1274
                                                                                                                                                                                                                                                                                                                     ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
                                                            GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTT
                                                                              gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                                                                                                                                                       tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
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_YLINKER ECORI-ClaI-ECORV-XbaI-BglII-XhOI-SacI-NruI-HindIII
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1- 235
230- 268
263-2668
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MARY pIC7 #length 2668 |
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/db_xref="taxon:32630"
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polylinker of pIC7
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DATE 17-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. pUC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artificial sequence.
1 (bases 1 to 2674)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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SOURCE artific
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     VecBase(3):pUC8, VecBase(3):pUC9, VecBase(3):pUR222 PARENT Features of pUC7 (2674 bp)
                                                        #parent
VecBase(3):pBR322, VecBase(3):M13mp7,
ConBank(50):EcoLac, VecSource(3):bGa17
                                                                                                                                                                                             Assembled from pUC19 and M13mp7 by F. Pfeiffer, MPI, Martinsried Revised 16-DEC-1986 by F. Pfeiffer:
2296/7 'AT' to 'TA' to match revised sequence of PBR322
The strand shown contains the beta-galactosidase mRNA sequence including the multiple cloning site of M13mp7.
                                              offspring#
                                                                                                                                                                                                                                                                                                                                                                                                     #authors Vleira J., Messing J.
#journal Gene (1982) 19: 259-268
#comment see walso 'note added in proof'
                                                                                                                                                                                                                                                                                                                   #comment vector I-A-iv-20
                                                                                                                                                                                                                                                                                                                                #authors Pouwels P.H., Enger-Valk B.E.,
                                                                                                                                                                                                                                                                                                                                                                             #number 2
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residue
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Best Local :
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                                                                                                                      1039 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
                                                                                                                                                                                                                                              1159 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
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                                                                                                                                                                                                    421 ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcgggggggaaaactc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                        481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
                                                                                                                                                                                                                                                              361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                                                                                                                                                                                                                                                                                     241 agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 100.0%; Score 1001; DB 12; Length 2674; Local Similarity 100.0%; Pred. No. 1.2e-274;
gccgcaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                                                                                      AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
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#indicator beta-galactosidase
MMARY pUC7 #length 2674 |
Location/Qualifiers
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mut 1116 T C 3912 (c) pBR322
mut 1417 A G 3611 (c) pBR322
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(c) pBR322
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                                                                            gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga
                         CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1346
                                                                                                                                            cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
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pUC13 DNA sequence.
A02712
                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 8809373-A 10 01-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSION VECTOR FOR ADJUSTABLE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial sequence.
1 (bases 1 to 2680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct
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                                                                                                                                                                                                                                                                                            h 100.0%; Score 1001; DB 6; Length 2680; Similarity 100.0%; Pred. No. 1.2e-274;
                                                                                                                                                                                                                                                                                   Conservative
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683 c 676 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                                                                     Unpublished (1991)
These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. pUCl
                                                                                                                                                                                                                           Gilbert, W
                                                                                                                                                                                                                                                                          synthetic construct
                                                                                                                                                                                                                                                                                             Synthetic construct DNA.
                                                                                                                                                                                                                                                                                                                                                                                    SYNPUC12V
                                                                                       TITLE pUC12 - Cloning vector DATE 17-SEP-1986
                                                                                                                                       Cloning vector
                                                                                                                                                                                                         Obtained from VecBase 3.0
                                                                                                                                                                                                                                                            artificial sequence.
                                                                                                                                                                                                                                                                                                                                                  L09129
                                                                                                                      ENTRY PUC12
                REFERENCE
                                  SOURCE
                                                 ACCESSION VB0023
#number
                                                                     #sequence
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                                                                                                                                                                                                                                                                                                                                                                cloning
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                                                                     16-DEC-1986
                                                                                                                                                           of the GenBank Currator Program. pUC12
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BASE COUNT
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                                                       tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                           cgctcgtcgtttggtattggcttcattcagctccggttcccgacgatcaaggcgagttaca 180
agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
                                  TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1286
                                                                                                        CGCTCGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1346
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WARY pUC12 ,#length 2680
Location/Qualifiers
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pUC12. source

mut 1122 T C 3912 (c) pBR322

mut 1423 A G 3611 (c) pBR322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946-1734 1-789 Ap-R; b-lactamase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #resistance Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VecBase(3):pUC18, VecBase(3):pSP64, VecBase(3):pGEM1, VecBase(3):pSP6T3, VecBase(3):pT712, VecBase(3):pCKSP6 PARENT Features of pUC12 (2680 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembled from pUC18 and M13mp10 by F. Pfeiffer, MPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Vieira J., Messing J.
#journal Gene (1982) 19: 259-268
#comment see 'note added in proof'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #offspring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #brother
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsvier 1985 and supplements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #number 2
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1069-1297
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2351-2252
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Lac-Operon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atttagaaaaataaacaaataggggttccgcgcaccatttccccgaaaagtgccacctgac
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                                                                                     Gene
Unpublished
                                                                                                  The pUC plasmids, an M13mp7-derived mutagenesis and sequencing with synt
                                                                                                                                             artificial sequence; vectors 1 (bases 1 to 2680)
            Obtained
                           Gilbert, W.
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Cloning vector pUC13
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                                                                                                                                                                                                                             L09130.1 GI:310822
                                        (bases 1 to 2680)
                                                                                   19 (3), 259-268 (1982)
           from VecBase
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COMMENT
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                                                                                                                                                                                                                                                                                         POLYLINKER HindIII-PstI-SalI-XbaI-BamHI-SmaI-SacI-EcoRI SELECTION
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                                                                                                                                                                                                                                                                                                                                pUC13 source
mut 1122 T C 3912 (c) pBR322
mut 1423 A G 3611 (c) pBR322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Vieira J., Messing J.
#journal Gene (1982) 19: 259-268
#comment see 'note added in proof'
                                                                                                                                                                                                                                                                                                      946-1734 1-789 Ap-R; b-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #parent
VecBase(3):pUC9, VecBase(3):M13mp11, VecSource(3):bGal13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembled from pUC19 and M13mp11 by F. Pfeiffer, MPI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence
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                                                                                                                                                                                                                                                   #indicator beta-galactosidase
MARY pUC13 #length 2680
                                                                                                                                                                                                                                                                              #resistance
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542- 678
679-2680
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VecBase(3):pSP65, VecBase(3):pGEM2, VecBase(3):pT713 PARENT
satures of pUC13 (2680 bp)
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                                                                                                                        /note="Lac-operon"
233. .283
                                       /note="pBR322"
879. .1739
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1. .2680
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                             /note="Ap-R"
                                                                                 /note Lac-operon"
                                                                                                            /note="Ml3mpl1 polylinker"
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Query Match 100.0%;
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Matches 1001; Conservative (
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atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780
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LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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Search completed: January 8, 2002, 17:16:51 Job time: 12102 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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AAZ22020	.AAV39266	AAT78825	AAA51630	AAA51632	AAQ04655	AAZ99245	AAV43439	AAV32980	AAF59053	AAA74638	<b>I</b> D	
Nucleotide sequenc	Plasmid puches nuc	Kappa Light Chain	Plasmid peme/9 con	Plasmid pGM6/8 con	Plasmid protes enc	Nucleotide sequenc	DNA segeunce of th	Th/ target plasmid	Plasmid Vector put	Plasmid pSP72. Es	Description	

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AAX77614 AAX73291 AAZ22045 AAV03801 AAV03801 AAC82936 AAD09269	AAV170002 AAV39243 AAC21997 AAF55224 AAV12068 AAX77617	AAZ39628 AAF55225 AAV12067	AAF26076 AAF26094 AAC55541 AAQ04010 AAF59062	AAC48207 AAT69188 AAT69189 AAA51634 AAF26077 AAT58319	AAV 3924 2 AAT78801 AAZ21996 AAZ26078 AAX61041 AAV00679 AAV067942	AAD04947
Expression constru plasmid pHCGG5 nuc Nucleotide sequenc Retroviral vector Transdominant effe pCMV-I-Cre-pA vect	Plasmid pCG7-96 nu Nucleotide sequenc Nucleotide sequenc Murine IAd beta ch Expression constru	DNA sequence of produced in the Nucleotide sequence Murine IAd alpha commander the New Yorkain	Feiine IL-12940 en Plasmid pMol-fill2 attR reading frame Plasmid pSUN387. Plasmid pUN387-6h73	Construct pGEM-hTR Construct pGEM-hTR Plasmid pGM712 con Feline IL-12p35 en DNA sequence of he	ight cha ide segu IL-16 en pFA6-Ka pTRH43 pND211	Plasmid pRK50 used

## ALIGNMENTS

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AAA74638
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                             Plasmid pSP72; NSE-p25 transgene; p25; cdk5 activator; neuron specific enclase; NSE; promoter; neurodegenerative disease; nativateral sclerosis; Alzheimer's disease; parkinson's disease; amyeLolateral sclerosis; Huntington's disease; traumatic brain hojury; stroke; transgenic animal; Huntington's disease; traumatic trau hyperphosphorylation; ds.
                                                                                                                                                                                                                                                           spinocerebellar degeneration; tau hyperphosphorylation;
                                                                                                                                                                                                                                                                                                                                                                          05-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    AAA74638;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAA74638 standard;
                                                                                                                                                                                                                                                                                                                                             Plasmid pSP72.
New recombinant DNA molecule comprising gene encoding p25, useful for producing transgenic animal to serve as model for \ensuremath{\mathsf{E}}
                                                                                                                         03-FEB-1999;
                                                                                                                                                                                09-AUG-2000.
                                                                                                                                                                                                                                   Escherichia coli.
                                           WPI; 2000-507252/46.
                                                                  Ahlijanian MK, Mcneish JD;
                                                                                             (PFIZ ) PFIZER PROD INC
                                                                                                                                                   02-FEB-2000; 2000EP-0300797.
                                                                                                                                                                                                          EP1026251-A2
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                                                                                                                          99US-0118478
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                2462 BP.
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The present sequence is the commercially available plasmid pSP72. The CS SV40 polyadenylation sequence, the rat neuron specific enclase (NSE) promoter and the human cDNA for p25 were cloned into plasmid pSP72 to GC generate the NSE-p25 transgene. This was used in the production of CC cdx5. Overexpression of p25 is sufficient to produce hyperphosphorylation CC of tau, which is seen in the neurofibrillary tangles associated with CC Alzheimer's disease. The transgenic animals are useful as in vivo systems CC for screening potential therapeutic compounds for their ability to CC inhibit or prevent the production of hyperphosphorylated tau and CC associated neuronal death. The transgenic animals are suitable for use as disease models of neurodegenerative diseases and tau-related pathologies, CC such as Alzheimer's disease, parkinson's disease, amyelolateral CC sclerosis, Huntington's disease, stroke, traumatic brain injury, CC spinocerebellar degeneration. They are also useful as models of cdk5/p25 and tau biochemistry, and to establish the role of the human p25 in the formation of hyperphosphorylated tau in neurodegenerative conditions.
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    0; Mismatches

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                            Query Match
Best Local Similarity
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Db

Sequence 2686 BP; 661 A; 685 C;

675 G;

665 T; 0 other;

100.0%;

Score Pred.

No. 1001;

1; DB 22; 3.5e-263;

Length

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                                 The present invention describes a peptide, its complex, derivative or its polymerizate, where the peptide (I) has a formula of: alpha1-alpha2-alpha3-alpha4-alpha5-alpha6-alpha7 where alpha1 to alpha7 = amino acid sequence selected from amino acid sequences ranging from 11-19 amino acids derived from T cell epitopes derived from cedar (japanese cedar - Cryptomeria japonica) pollen allergens. The peptide can be used in an antisugipollinosis agent. AAF59011 to AAF69062 and ABB69094 to AAB69121 represent sequences used
                              ij
                                                                                                                                                                                                                                            WPI; 2001-185061/19.
                                                                                                                                                                                  Example 11;
                                                                                                                                                                                                             Novel peptide and its use
                                                                                                                                                                                                                                                                                                                     15-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese cedar; Cryptomeria japonica; cedar pollen allergen; T cell epitope; antisugipollinosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid vector pUC18M5 nucleotide sequence SEQ ID NO:70.
                                                                                                                                                                                                                                                                       (HAYB ) HAYASHIBARA SEIBUTSU (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000JP-0071710.
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                         exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
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AAV32980 standard; DNA; 3190 BP.

target plasmid sequence.

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACATAGCAGAACTTTAMAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
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                                                                                                                                                          atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac
                                                                                                                                                                                                                                          CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT
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GCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGC 531
                                             ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA 572
                                                          acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                                                                              TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                          GTCTAAGAAACCATTATTATCATGACGATTAACCTATAAAAATAGGCGTATCACGAGGCCC
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RESULT 3 AAV32980/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transposon(s) encoding mutant ATP using proteins for insertion which is efficient and random, with reduced site specificity; for DNA sequencing and altering gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3190 BP; 784 A; 808 C; 773 G; 825 T; 0 other;
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                                                                                            gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga
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                                         agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
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                                                                                                                                                                             recA gene; extein; screening; antimicrobial activity; intein; protein splicing element; growth protein; antimicrobial agent;
           (HEAL-) HEALTH RES INC. .
                                                                                          18-AUG-1998
                                                                                                                  US5795731-A
                                                                                                                                                                                                                      DNA sequence of the vector pGEM3-2f(-).
                                                               26-AUG-1996;
                                                                                                                                                                                                                                                                                                      AAV43439 standard;
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                                                                                                                                                                      splicing; identification;
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Best Local Similarity
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                   541 tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaacaggaaggcaaaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening agents for antimicrobial activity - by monitoring affect of splicing intein into reporter gene, also useful for studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 6B; 64pp; English.
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tottoagcatottttactttcaccagcgtttctgggtgagcaaaacaggaaggcaaaat 2132
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                                                                                 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 A; 817 C; 805 G; 838 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1001; DB 19; Length 100.0%; Pred. No. 3.7e-263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PinPoint vector; fusion protein antigen; membrane antigen; syphilis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ99245 standard; DNA; 3331 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of a PinPoint expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2000 (first entry)
                        the course of the invention. The specification describes a method for detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnosis of syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                        EP985931-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum.
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                                                                                                                                                                      Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo
                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                              12-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2000
                                                                                                                                         Disclosure; Page 8-9; 16pp; English.
                                                                                                                                                                                                                                                           Mullenix MC,
                                                                                                                                                                                                                                                                                      (BECT ) BECTON DICKINSON & CO
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                                                                                                              present sequence represents the PinPoint vector, which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcgggtgttggcgggtgtcggggtgggcttaactatgcggc 1001
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                                                                                                                                                              GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                                                                     gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
                                                                                                                                                                                                                  ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
                                                                                                                                                                                                                                 atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac
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             gcgggtgttggcgggtgtcggggctggcttaactatgcggc 1001
                                                                 acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca
                                                                                                        TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                                        GCGGGTGTTGGCGGGTGTCGGGGCTTGGCTTAACTATGCGGC
                                                    ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCCGTCAGGGCGCGTCA
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Pred. No. 3.7e-263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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AAQ04655/c
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        1948
                                                                                                                                                                       2128
                                                                                                                                                                                                                  2188 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2129
                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding the Fd chain of antibody MAK33 were used to transform E. coli DSM 3689 and the resulting cells grown to form inclusion bodies. After the final renaturation step an 18% Yield of biologically-active protein was
                                                                                                                                                                                                                                                                                                                                               Sequence 3343 BP; 815 A; 871 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activated antibody prodn. from recombinant procaryotic cells by solubilisation under reducing conditions, then oxidative renaturation, carried out at low protein concn.
                                                                                                                                                                                                                                                                                                                                                                             see also AAQ04654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rudolph R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEF ) BOEHRINGER MANNHEIM GMBH.
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                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                 1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT 1889
             agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctctttact 300
                                                                                                      cyctcytcytttyytattyycttcattcayctccyyttcccaacyatcaayycyayttaca 180
                                                                 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                             AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA
                                                  TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1949
                                                                                                                                                                             agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88DE-3835350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= Fd chain of MAK33
                                                                                                                                                                                                                                                                                        100.0%; Score 1001; DB 11; 100.0%; Pred. No. 3.8e-263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lenz H;
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                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                            846 G; 811 T; 0 other;
                                                                                                                                                                                                                                                                                                  DB 11; Length 3343;
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                                                                                                                          Uridine phosphorylase; udp; purine nucleoside phosphorylase; PNP; deo Genetically modified organism; catalyst; transglycosylation; nucleoside analogue; alpha-pentose-1-phosphate sugar; phosphorolysis; anti-tumour; mesophilic bacterium; ss.
                                                      misc_RNA
                                                                                                                                                                                             Plasmid pGM678 containing E. coli deoD gene.
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                                                                                             Synthetic.
                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                               AAA51632 standard;
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               /label= pUC18_sequence
216..952
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                                                                                                                                                                                                                                                                                                                                                                                                                      come or more nitrogen atoms, for preparing alpha-pentose-1-phosphate come or more nitrogen atoms, for preparing alpha-pentose-1-phosphate comparing hypha-pentose-1-phosphate and sugars by phosphorolysis reactions and for producing nucleosides and commodified nucleosides are used directly or as intermediates in the preparation of comparing the comparing control of the comparing control of the comparing control of the comparing control of the comparing the comparing comparing at least one gene sequence of a mesophilic bacterium coding comparising at least one gene sequence of a mesophilic bacterium coding comparising at least one gene sequence of a mesophilic bacterium coding comparising at least one gene sequence coding for antibiotic resistance. In particular, the coli udp and deod genes are used. Recombinant strains produced consing the vectors express polypeptides with enzyme Udp and PNP activity in large amounts, e.g. 340-1040 times higher Udp activity and 120-200 control of the comparing control of the comparing wild type activity than non-transformed corresponding wild type
                                                                                                                                                                                                                                                                                                       Matches 1001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalysts of transglycosylation reactions between a donor nucleoside an acceptor base, for preparing nucleoside analogues containing heterocyclic systems with purine and/or pyrimidine bases substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Host cells genetically modified to express uridine phosphorylase (UdP) and purine nucleoside phosphorylase (PNP) or their corresponding crude or purified extracts, either separately or in combination are used as
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                                                                                                                                                                                 2168
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                 AGTTCGCCAGTTAATAGTTTCCCCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA
                                                                                                                     CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA
agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
                                                       TGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
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                                                                                                                                                                                                                                                                                                     100.0%; Score 1001; DB 21; 100.0%; Pred. No. 3.8e-263; Live 0; Mismatches 0;
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                                                                                                                                                                          Uridine phosphorylase; udp; purine nucleoside phosphorylase; PNP; deoD; Genetically modified organism; catalyst; transglycosylation; nucleoside analogue; alpha-pentose-1-phosphate sugar; phosphorolysis; anti-viral; anti-tumour; mesophilic bacterium; ss.
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                                                              misc_RNA
                                                                                                                       Synthetic
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                                                                                                                                         coli.
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                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               CC Host cells genetically modified to express uridine phosphorylase (UdP)
CC and purine nucleoside phosphorylase (PNP) or their corresponding crude or
CC purified extracts, either separately or in combination are used as
CC catalysts of transglycosylation reactions between a donor nucleoside and
CC an acceptor base, forpreparing nucleoside analogues containing
CC heterocyplic systems, with purine and/or pyrimidine bases substituted by
CC one or more nitrogen atoms, for preparing alpha-pentose-1-phosphate
CC sugars by phosphorolysis reactions and for producing nucleosides and
CC modified nucleoside analogues (all claimed). The modified or natural
CC nucleosides are used directly or as intermediates in the preparation of
CC drugs with anti-viral and anti-tumour activity and for preparing
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC the E. coli udp and deoD genes are used. Recombinant strains produced
CC using the vectors express polypeptides with enzyme UdP and PNP activity
CC times higher PNP activity than non-transformed corresponding wild type
CC strains.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Matches 1001;
                                                        2109
                                                                                                                               2169
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                                                                                                                    cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
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AAV39266
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                                                                                                                                                                                                                                                                                                                                                                        Transgenic animal; human heterologous antibody; transgene; D4 binding; isotype switching; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1816
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                                                                    Hybridoma producing antibody specific for interleukin-8 - prevent efflux of neutrophils from vasculature, and treat
                                                                                                                                                                                                                                 01-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                             cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pLC6G5 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV39266 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcctttt
                                                                                                                WPI; 1998-333306/29.
                                                                                                                                                                                                    02-DEC-1996;
                                                                                                                                                                                                                                                              11-JUN-1998
                                                                                                                                                                                                                                                                                           WO9824884-A1
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                           Example 42; Pages 317-319; 452pp; English.
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                                                                                                                                           Lonberg N;
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The present sequence represents a plasmid, pLC6G5,

which contains

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synthetic kappa light chain sequence (created using oligonucleotide AAV39244-65). This synthetic sequence differs from natural sequences in that strings of repeated oligonucleotides are interrupted (to facilitate oligonucleotide synthesis and PCR amplification), optimal translation initiation sites are incorporated and Hindri sites were engineered upstream of the translation initiation sites. The plasmid is used in the construction of minigenes for expression of IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes is the transgenes are capable of production and the second of the second of the construction of the transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes
injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The anti-IL-8 antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and or constant region gene segment. The gene segments are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from vasculature. It can also be used to treat reperfusion
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947 A; 1015 C; 912 , G; 945 T; 0 other;

Query Match

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Pred. No. 3.9e-263;
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producing a heterologous antibody. The antibodies are isolated form hybridoma, comprising B cells, that is obtained from a transgenic me having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells The specification describes transgenic animals that are capable

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                                                                                                                        Novel transgenic
                                                                                                                                                                                                                                                                                                                                                                                              Transgenic animal; heterologous antibody; hybridoma; B cell; transgenic mouse; human heavy chain transgene; digoxin; human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2056
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                                                                                 Example 42;
                                                                                                                                                       WPI; 1999-551219/46
                                                                                                                                                                                                               (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                           13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection; blood disorder; coagulation disorder;
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                                                                                                                                                                                                                                                                      12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of plasmid pLC6G5.
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                                                                                 Page
                                                                                                                                                                                  Fishwild DM,
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                                                                                                                                                                                                                                                                      99WO-US05535
                                                                              318-320; 484pp; English.
                                                                                                                          non-human animals used to
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                                                                                                                          produce heterologous
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                                                                                        The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition sequences (RRSs) specific to site specific recombinase which is capable of unidirectional inversion of double standard DNA segment. One of the DNA segment (disruption cassette) is inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional orientation of the gene to be trapped. The coll comprising the gene trapping construct is useful for the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is
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                                         useful to study gene function at various developmental stages. The generapping construct is useful for mutationally inactivating all cellulations. The present sequence is pRK50 vector, which is used to test Cre
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direction relative
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27-OCT-1999;
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                               recombinase mediated inversion, which is related to the
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Local Similarity

100.0%; ilarity 100.0%; Conservative

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Score 1001; DB 19; Pred. No. 4e-263; ; Mismatches 0;

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RESULT 13
AAV39242
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                                                                                                                                                      The present sequence represents the kappa light chain plasmid, pCK7-96, which includes the kappa constant region and polyadenylation site. The CC plasmid is used in the construction of minigenes for expression of CC Igdkappa anti-CD4 antibodies, in the transgenic mouse of the invention. CC The specification describes transgenic non-human animals, especially a cc mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals cc have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a cc variable-diversity-junction (V-D-J) recombination. The transgenes include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and one constant cc animal. The antibody can be used to prevent eflux of neutrophils from cv asculature. It can also be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The canimal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybridoma producing antibody specific for interleukin-8 - prevent efflux of neutrophils from vasculature, and treat
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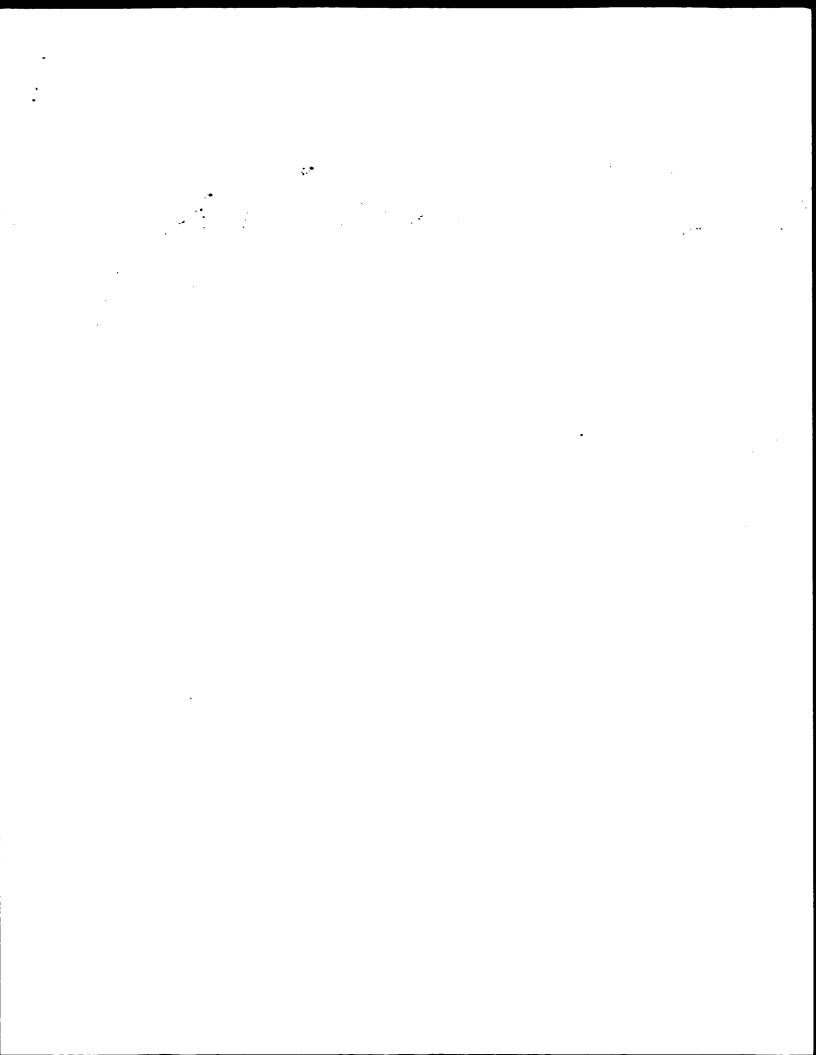
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A novel composition has been developed which comprises an immunoglobulin (19) having an affinity constant (Ka) of at least 2 multiply 1000000000 M-1 for binding to a predetermined human antigen. The present sequence represents the kappa light chain plasmid pCK7-96 which includes the kappa constant region and polyadenylation site. Anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals produce a first 1g type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent heterologous
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Pred. No. 4e-263;
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 13-MAR-1998;
                             12-MAR-1999;
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Best Local
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	601 1756 661 1816 721 721 1876 781 1936 841 1936 901 901 901 901
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Search completed: January 8, 2002, 17:27:47 Job time: 12647 sec



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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                            Database :
                                                                                                                                                                                      Post-processing: Minimum Match 0%
              IDENTITY_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January 8, 2002, 17:19:07; Search time 177.22 Seconds
                                                                                                                                                Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                      351203 seqs, 11,3238999 residues
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1001
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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1279.226 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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26 27	21 22 24	17 18 19 20	14 15 16	12	987654	NO. 1 2 3
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100.0	100.0	100.0	100.0	100.0 100.0 100.0	100.0 100.0 100.0 100.0	Query Match Length 100.0 3104 100.0 3104 100.0 3343
4723 4723 4926	4622 4622 4696	3908 1 3908 1 4045	3883 3883	3878 • 3878 3881 3881	3819 3875 3875 3875 3875 3876	3104 1 3104 1 3343 6
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28 1001 100.0 4926 4 US-08-758-417A-268 29 1001 100.0 4950 3 US-08-758-433F-58 20 1001 100.0 5181 2 US-08-929-967-16 20 30 1001 100.0 5181 3 US-08-801-344-5 21 1001 100.0 5181 4 US-08-801-344-5 21 1001 100.0 5181 4 US-08-8793-610-3 33 1001 100.0 5294 2 US-08-793-610-3 34 1001 100.0 5294 2 US-08-793-610-3 35 1001 100.0 5323 2 US-08-793-610-1 36 1001 100.0 5364 2 US-08-793-610-4 37 1001 100.0 5364 2 US-08-793-610-4 38 1001 100.0 5865 4 US-09-011-745-8 39 1001 100.0 5865 4 US-09-011-745-8 40 1001 100.0 6061 4 US-09-011-745-6 41 1001 100.0 6280 3 US-08-893-327-15 42 1001 100.0 6280 3 US-08-893-327-17 43 1001 100.0 6280 3 US-08-893-327-17 44 1000 100.0 6280 3 US-08-893-327-17 45 1001 100.0 6280 5 PCT-US94-00658-1
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3 US-08-758-417A-268 3 US-08-798-33F-58 2 US-08-929-957-16 3 US-08-801-344-5 4 US-09-498-599-5 2 US-08-793-610-2 2 US-08-793-610-2 2 US-08-793-610-4 3 US-09-175-690A-1 4 US-09-175-690A-1 4 US-09-171-745-6 3 US-09-011-745-6 4 US-09-011-745-6 3 US-08-893-327-15 3 US-08-893-327-17 3 US-08-893-327-17 5 PCT-US94-00658-1
US-08-758-417A-268 US-08-793-33F-58 US-08-929-967-16 US-08-801-344-5 US-08-793-610-3 US-08-793-610-1 US-08-793-610-1 US-08-793-610-4 US-09-011-745-8 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-09-011-745-6 US-08-893-327-15 US-08-893-327-17 US-08-893-327-19 US-08-893-327-19 US-08-893-327-19 US-08-893-327-19

## ALIGNMENTS

US-07-415-307A-1

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US-07-415-307A-1
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                                                                                                                                                                                              FILING DATE: 19900109
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP89/0026
FILING DATE: 12-Jan-1989
APPLICATION NUMBER: DE 38 00 642.1
FILING DATE: 12-Jan-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
APPLICATION TORNATION:
NAME: HANSON, NO. 5344757man D.
REGISTRATION NUMBER: BOER 798
REFERENCE/DOCKET NUMBER: BOER 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISActte, 5
COMPUTER: IBM PS/2
COPERATING SYSTEM: PC/DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holtke, Hans Joachim
APPLICANT: Scibl, Rudolf
APPLICANT: Schibltz, Gudrun
APPLICANT: Scholer, Hans
APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for the Detection of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                     TELEPHONE: 212-0-
TELEPHONE: 212-838-3884
THO TD NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: 19900109
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                                  STRANDEDNESS:
                   TOPOLOGY:
                                                                           LENGTH:
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                                                      NUCLEIC ACID
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                                                                           3104 base pairs
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                                       single
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Matches 1001;
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                                                                                                                     acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca
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               GCGGGTGTTGGCGGGTGTCGGGCTTGGCTTAACTATGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
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               2549
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1001; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08371320 Patent No. 5702888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/415,307
FILING DATE: 09-Tan-1990
APPLICATION NUMBER: PCT/EP89/0026
FILING DATE: 12-Tan-1989
APPLICATION NUMBER: DE 38 00 642.1
FILING DATE: 12-Tan-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                               NAME: Hanson, No. 5702888man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: BOER 7 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200
                                                                                                                                1609 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC/DOS
SOTTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/371,320
FILING DATE: 11-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holtke, Hans Joachim
APPLICANT: Seibl, Rudolf
APPLICANT: Schmitz, Gudrun
APPLICANT: Schmitz, Gudrun
APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for the Detection
                                                                  121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
181 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                 61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                              CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3104 base pairs
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 1001; DB 1; 100.0%; Pred. No. 2.1e-301;
                                                                                                                                                                                                                                                                                                        0;
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APPLICATION NUMBER: US/08/20
FILING DATE: 02-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 942,370
FILING DATE: 09-SEP-1992
APPLICATION NUMBER: 498,500
FILING DATE: 23-MAR-1990
APPLICATION NUMBER: 76,207
FILING DATE: 23-OCT-1986
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                                                                                                                   APPLICANT: RUDOLPH, RAINER; FISCHER, STEI
TITLE OF INVENTION: PROCESS FOR THE ACTI
AFTER GENETIC EXPRESSION IN PROKARYOTES
NUMBER OF SEQUENCES: 4
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                                                                                                          CURRENT APPLICATION DATA:
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Local Similarity 100.0%;
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                                                     tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag
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                                            TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 10-OCT-1996
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER US 08/544,404
FILING DATE: 10-OCT-1995
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APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
                                       PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 16-DEC-
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APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
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FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/161,739 FILING DATE: 03-DEC-1993
                                                                                                                                                                      APPLICATION NUMBER: US 01 FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 10-DEC
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 18-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 22-JUI
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IOR APPLICATION DATA:
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/209,741
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: San Francisco
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o. 6255458
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18-NOV-1993
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MBER: WO PCT/US96/16433
10-OCT-1996
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: U.
FILING DATE: 02-DC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W
                                                      1756 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTTTT
                                                                                                                                                                                                                                                                                   1576 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTC
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TELEPHONE: (415) 576-0200
TELEPAS: (415) 576-0300
TELEPAS: (415) 576-0300
FORMATION FOR SEQ ID NO: 393:
661 caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 720
                                                                                                                                                  541 tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaat 600
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                                                                                                                                                                                                                            481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
                                                                                                                                                                                                                                                                                                                                                                               361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcg
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies NUMBER OF SEQUENCES: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
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                               FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcaggggcgcgtca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/758,417A FILING DATE: 02-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/728,463 FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/165,699 FILING DATE: 10-DEC-1993
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/209,741 FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/544,404 FILING DATE: 10-OCT-1995
                                                                     FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
                                                                                                           FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
                                                                                                                                                                   APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993
REGISTRATION NUMBER: 41,303
                                                                                                                                                 APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                           FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/161,739
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                   Serafini,
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                 Andrew T.
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TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ
US-08-758-417A-243
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Best Local Similarity
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 243:
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781 gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
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LENGTH: 3819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                          TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
                                                      ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
                                                                         atttagaaaaataaacaaatagggttocgcgcacatttccccgaaaagtgccacctgac 780
                                                                                                                                                                                                                                                                      TCTTCAGCATCTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1755
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Pred. No. 2.3e-301;
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                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-MAR-1998 (CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OLSON, ARNE M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSR14710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3875 base pairs
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   2431 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 2372
                                                                      2491 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2432
                                                                                                                                                                                                                                                 HYPOTHETICAL: P
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MEDIIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA: 9
                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING
NUMBER OF SEQUENCES: 59
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CITY: Chicago
STATE: Illinoi:
COUNTRY: USA
ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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Pred. No. 2.4e-301;
                                                                                                                                            Mismatches
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Patent No. 6251627
                                                               GENERAL INFORMATION:
APPLICANT: Cai, Z
APPLICANT: Sprent
                  APPLICANT:
                                                    APPLICANT:
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   OF INVENTION:
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                                                                                                                                       Application US/09039641
            Jackson, Michael
Peterson, Per A
                                             Sprent, Jonathan
Brunmark, Anders
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 21:
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MEDIUM TYPE: Flopp# disk
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                                                                                                                                                                                                                                                                                                                                                                                                               2491 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2432
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HYPOTHETICAL: NO
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LENGTH: 3875 base pairs
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TELEPHONE: (312) 580-1180
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NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      2311 TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 8-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga 360
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APPLICANT: Cai, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09039762A Patent No. 6255073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1651 TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEPAX: (312) 580-1189
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                             ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,
                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                         FILING DATE: 16
CLASSIFICATION:
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    ZIP: 60606
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                               STATE:
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20 No. 6255073th Wacker Drive, 36th Floor
                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                   Floppy disk
                                                                                                                      16-MAR-1998
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                                                               30,203
                                                  TSRI 471.0 DIV.2
                                                                                                                                                                            Version
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3875 base pairs

21:

TYPE: nucleic acid STRANDEDNESS: double

MOLECULE TYPE:

TOPOLOGY:

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HYPOTHETICAL: NO
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                                GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                  ATTTAGAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC 1712
                                                                                                   atttagaaaataaacaaatagyggttccgcgcacatttccccgaaaagtgccacctgac 780
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Pred. No. 2
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                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09039982A
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                 MOLECULE
HYPOTHETICAL: NO
                                                                                                        2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3878 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cai, Zeling APPLICANT: Sprent, Jonathan APPLICANT: Brunmark, Anders
121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION
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                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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(312) 580-1189
                                                                                                                                                               Conservative
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                                                                                                                                                          100.0%; Score 1001; DB 4; 100.0%; Pred. No. 2.4e-301; ative 0; Mismatches 0;
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; ANTI-SENSE: US-09-039-641-27
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INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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FILING DATE: 8-MAR-1995
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                                                                                                                                                                                                                                                                                                                                       181
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361
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                                                                                                                                                                                                                                                                                                      AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 2375
                                                                                                                                                                                                                                                                                                                                                                                                cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                             ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
                                                                                                                       GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
                                                                                                                                        gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                  AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
                                                                                                                                                                                                                                                            agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
                                                             CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
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20 No. 6251627th Wacker Drive, Suite 3000
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US-09-039-762A-27/c

: Sequence 27, Application US/09039762A

: Patent No. 6255073
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APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                      SEQUENCE CHARACTERISTICS:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,203
                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION MATA:
APPLICATION NUMBER: US/09/039,762A
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM.
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               STREET: 20 No. CITY: Chicago STATE: Illinoi
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                                                                                                             REFERENCE/DOCKET NUMBER:
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3878 base pairs
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N: 435
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1654 TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                      1714 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                             1774 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
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HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                       2074 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
                 841 tttcgtctcgcgcgttttcggtgatgacggtgaaaaccttctgaccatgcagctcccggag 900
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                                                                                          781 gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
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STRANDEDNESS: double
TOPOLOGY: linear
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-9991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
OPERATING SYSTEM: PC.DOS/MS-DOS
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CLASSIFICATION:
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03-DEC-1993
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER:
FILING PT.
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ATTORNEY/AGENT INFORMATION:
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                                                 1696 TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1755
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601 gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
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US-08-758-417A-217
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/053,131 FILING DATE: 26-APR-1993
                                                                                   APPLICATION NUMBER: US 08/096,762 FILING DATE: 22-JUL-1993
                                                                                                                                   APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993
                                                                                                                                                                          APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-CCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/209,741 FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/728,463 FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                             APPLICATION
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                        NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA ; SEQUENCE DESCRIPTION: SEQ ID NO: 217: US-08-758-417A-217
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                                                               1756 GCCGCAAAAAAGGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTCCTTTTT 1815
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                                                                                                                                                                                                                                                                                                                           TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA 1695
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                         TCTTCAGCATCTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                   CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
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LENGTH: 3881 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415)
TELEFAX: (415) 57
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REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Serafini, Andrew T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-DEC-1992
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DB 4; Length 3881; Indels

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                                                                                                                 US-09-039-982A-30
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OLSON, ATNE M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEPAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Patent No. 6225042
                                                      Matches
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      2499
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APPLICATION NUMBER: US,
FILING DATE: 16-MAR-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2116
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                                                                                                                           ANTI-SENSE:
                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cai, Zeling APPLICANT: Sprent, Jonathan
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STREET: 20 No. 6225042th Macker Drive,
CITY: Chicago
STATE: Illinois
                                                             Local
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
  LENGTH:
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                                                               Similarity
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Application US/09039982A
225042
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                                                 Score 1001; DB 4;
Pred. No. 2.4e-301;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM AND METHODS FOR ACTIVATION OF T-CEL
                                                                         Length 3883;
                                                    Indels
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                                                 Gaps
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Sequence 30, Application US/09039641
Patent No. 6251627
GENERAL INFORMATION:
APPLICANT: Cal, Zeling
APPLICANT: Sprent, Jonathan
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ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
                                                      atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac
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; ANTI-SENSE: US-09-039-641-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEPAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1001; DB 4; Best Local Similarity 100.0%; Pred. No. 2.4e-301; Matches 1001; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jackson, APPLICANT: Peterson, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     2379
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LENGTH: 3883 base pairs . .
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NAME: Olson, Arne M.
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FILING DATE: 8-MAR-1995
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Search completed: January Job time: 12274 sec 8 2002, 17:20:23

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT ORIGIN	RESULT 1 AR138378 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	444444451555 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Result No. Sc
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Couto, L.B., Colosi, P.C. an Adeno-associated vectors f cells
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Couto,L.B., Colosi,P.C. and Qian,X.
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 Score 736.2; DB 6;
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AR071306
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Hybrid proteins with modified activity
Patent: US 5910481-A 1 08-JUN-1999;
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                                                           Sequence 1 from patent US AR112722
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Pred. No. 8.9e-155;
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US 6130203.
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Hybrid proteins with modified activity
Patent: US 6130203-A 1 10-0CT-2000;
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8831)
Danieru,J.K., Richiyaado,M.R., Goodon,A.B. and Uiriamu,A.U. MANUFACTURE OF FUNCTIONAL VIII FACTOR
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Homo sapiens
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JP 1985243023-A/2.
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Best Local Similarity
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                                              672 cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
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AAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACATCGCTAAGCCAAGGCCAC
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GENERIECH INC

OS Homo Sapiens
PN JP 1985243023-A/2
PD 03-DEC-1985
PF 19-APR-1985 JP 1985085295
PF 20-APR-1985 JP 1985085295
PR 20-APR-1984 US 84 602312
PI DANIEDU JIEFURII KEIPON, RICHIYAADO
ARRN BILHAA,
PI UIRIAMU AAUIN UTSUDO
PC C12N5/00/C12P21/00,(C12N5/00,C12R1
CC 12N5/00/C12P21/00,(C12N5/00,C12R1
CC 12N15/00/C12P21/00,(C12N5/00,C12R1
CC 212N15/00/C12P21/00,UC12N5/00,C12R1
CC 450urce: chical: No;
CC 450urce: cell_line=CH-2;
CC *Source: cell_line=CH-2;
CC *Source: cell_line=CH-2;
CC *Source: cell_line=CH-1;
FT 5'UTR
FT 5'UTR
FT CDS
Product='factor VII
FT CDS
Product='factor VII
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FT DolyA_signal 8948.8953
FT PolyA_site 8968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 125
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03-DEC-1985
19-APR-1985 JP 1985085295
20-APR-1984 US 84 602312
DANIERU JTEFURII KEIPON, RICHIYAADO MAAKU ROON, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UIRIAMU AAUIN UTSUDO
A61K37/04,A61K35/12,A61K35/74,C07H21/04,C07K13/00,C07K15/04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N15/00//C12P21/00, (C12N5/00, C12R1:91);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
1865 c 1800 g 235
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96.2%;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 590.6; DB 6; Length 8831; Pred. No. 2.5e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product='factor VIII'
110. .7265
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.7262
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/product='factor VIII'
7266. .<8967
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Methods of reducing factor viii clearance
Patent: WO 0071714-A 1 30-NOV-2000;
The American National Red Cross (US)
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AX052730
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VAKKEPKTWATY TAAEEEDWDYAPLULAPDDRSYKSQYLNIGORGI IGRYKKVREMAY
TDETERTREAJOHESGI LIGPLLYGEVGDTLLI I FKNGASERYNI YPHGITDVRPLYSR
RLPKGVKHLKOPP I LPGE I FKYKWTVTVEDGPTKSDPRCLTRYYSSFVNMERDLASGL
IGPLLICYKESVDQRCNOIMSDKRIVILFSVEDENRSWYLTENIQRFLPNPAGVQLED
PEFQASINIMBSI URGVYEDSLQLSVCLHEVAYWYLLS I GAQTDPLSVFFSGYTFKHKMV
YEDTLTLEFFSGETVFMSMENFGLWILGCHNSDFRNRCMTALLKVSSCOKNTGDYYED
SYEDLSAYLLSKNNALEPRSFSQNSHRRSTROKOFNATTI PEMDI EKTDPWFAHRTPM
PKIQNVSSDLLMLLRQSTPTHGLSLSDLOGAKVETFSSDPSGNLLISTI PEMDI EKTDPWFAHRTPM
PKIQNVSSDLLMLLRQSPTPHGLSLSDLOGAKVETFSSDPSGNLLISTI PENDLEKTNOSKLLESGLM
NSQESSWRKVYSTESGRLFFKGKRAHGPALLTKDNALFKVSI SILKTNKTSNNSATNR
KTHIDGPSLLI ENSPSVWQNI LESDTEFKKVTFLI HDRNLLFKVSI SLLKTNKTSNNSATNR
KTHIDGPSLLI ENSPSVWQNI LESDTEFKKVTFLI HDRNLMDRNATALELNHMSIKTT
SKNNEMVQOK KEGPI PEDAQNPDMSFFMLET LASARWID RRHGKNSLNSGOGPSPK
QLVSLJGPEKSVEGQNELSENKUVVGKGEFFTRDVGLK LEWFPSSRNLFLTUNDNLHEN
NTHNOEKKY I OEBI EKKETL I OENVVLOG I HTVTGTKNEMKNLFLSLSTRONVEGSYDGA
YAPVLODFRSLNDSTNRTKHITAHESKKGEEENLEGLGNOTKOI VEKYACTTRI SPNT
YNDOEN TO TOTHE TO TOTHE TO THE TOTHE TOTHE TOTHE TOTHE TOTHE
                        ENTYLPKPDLPKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGSLLQGTEGAI
KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
                                                                                                                   SQQNFVTQRSKRALKQFRLPLEETELEKRIIVDDTSTQWSKNMKHLTPSTLTQIDYNE
KEKGAITQSPLSDCLTRSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHLP
AASYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMTGDQREVGSLGTSATNSVTYKKV
ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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/db_xref="GI:12226921"
/translation="MQIELSTCFFLCLLRECFSATRRYYLGAVELSWDYMQSDLGELP
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mat\_peptide BASE COUNT 28 ORIGIN Matches 605; Query Match Best Local 372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431 Local Similarity aaaagactotgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac aagtcttccctggttggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag 971 CACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGA AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA AAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAAAAGAAGATGATA TGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAG Unknown Sequence 1 from 171409 Unknown Unclassified. 171409.1 Conservative APTKDEFDCKAMAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
IFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYLMDTLDGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEFXKMALYNLYFGVFETVENLPESKAGIWR
VECLIGEHLHACMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAMSTKFPFSWIKVDLLAPMIHGIKTQGAPQKFSSLYISOFIINYSLDGKKWQ
TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIARYIRLFTHYSIRSTLMELMGCDL
NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAMRPQVNNPKEW
LQVDFQKTMKVTGCTTQGVKSLLTSMYVKEFLLSSSQDCHQWTLFFQNGKVKYVFQGNQ DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY" GI:3007544 59.1%; 96.2%; 8967 bp patent US 1833 0; Score 590.6; Pred. No. 2.5 Mismatches g 5681746 2395·t ; DB 6; Length 8967; Indels 03-APR-1998 0; Gaps 425 305 611 185 485 791 731 365 671 665 605 911 545 0;

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                                                                                                                                                                                                                                                                                                                                                                                  tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
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Retroviral delivery of full length factor VIII
Patent: US 5681746-A 1 28-OCT-1997;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 8967)
Wood,W.I., Capon,D.J., Simonsen,C.C., Eaton,D.L., Gitschier,J.,
                                                     Homo sapiens
                                                                           factor VIII; signal peptide
                                                                                        X01179.1 GI:31498
                                                                                                                Human mRNA for
                                                                                                                          HSFVIIIR
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PKIQNYSSOLLMILLROSPT PHGLSLED LOCACKY ETF SDDYSPOALDEN MILTST 19ENDLEKTDPWFAHRTPM
PKIQNYSSOLLMILLROSPT PHGLSLED LOCACKY ETF SDDYSPOALDEN LIST 19ENDLA
AGTDNISSLGPPSMPHYDSOLDTILFOKKSSPLTESGEPLSSENNLST 19EDNLA
AGTDNISSLGPSMPHYDSOLDTILFOKKSSPLTESGEPLSGELMINSKLLESGLM
NSOESSWGKNVSSTESGELFKGKRAHGFALLTKNALTKY SISLLKTNKTSNNSATNR
KTHIDGPSLLIERSPSWPON LLESDTEEFK KVPPLIHDBHLMDKNATALRELHNSNKTT
SSKNMENVOOKKEGP 19PAQNPDMSFFKNJFLLPESARWIQRTHGKNSLNSGGPSPK
QLVSLGPEKSVEGQNELSEKNKVVVGKGFFKNJFLLSGLGNOTKQIVEKYACTTRISPNT
SSKNMENVOOKKEGP 19PAQNPDMSFFKNJFLLPESARWIQRTHGKNSLNSGGPSPK
QLVSLGPEKSVEGQNEFLSEKNKVVVGKGFFKNJFLLSTRONVEGSYDGA
YAPVLODFRSLNDSTNRTKKHTAHFSKKGEEENLEGLGNOTKQIVEKYACTTRISPNT
SQONFVYGRSKARLKOFFLLEETLEKRII TVDDTSTOMSKNMKHLIPSTLTOIDVNE
KEKGALTGSPLSDCLTRSHSIPOANRSPIPIAKVSSFPSIRPIYLTRVLFODNSSHLP
AASYRKKDSGVOESSHFLOGAKKNNLSLAILTLEAMONNYGTOIPKEEWKSOEKSPEKA
EKKATTIGSPLSDCLTRSHSIPOANRSPIPIAKVSSFPSIRPIYLTRVLFODNSSHLP
AASYRKKDSGVOESSHFLOGAKKNNLSLAILTLEAMONNYGTOIPKKV
ENTVLKPDLLFKTTSGKVELLFKHIYOODDENOSFRSOKKTHRYFIAAVERLH
PKKNDTILSLNACESNIAIAALNEGQNKPELEVTWAKGGRTEELCSQNEPVLKRHQRE
ITRTTLOSDOESSNALIAALNEGQNKPEIEVTWAKGGRTEELCSQNEPVLKRHQRE
ITRTTLOSDOEDINDDTISVEMKKEDEDIYDEDENOSFRSOKKTHRYFIAAVERLH
DYGMSSSPHVLRNAQSGSVPOFKKVVEDETDLOSFTOPLYRGELNEHLGELGPYIRA
EVEDNIAWTFRNOASRPYSFYSSLISYEEDORGGAEFRKNEVKPNETKYYFWRYOHHM
APTKDEFROWTSTROAGSPOYSFYSSLISYEEDORGAEFRKNEVKPNETWALTERAAGTHD

FKKKDTILGTHAANSTROAGSONDERDYFKNENKETWANIAUGYIMDTLDGLVNAQDOR
ITPOETKSWTFTRNOASRPYSFYSSLISYEEDORGAEFRKNEVKANTOKYNDHLOGLOPPILEF
TETTLOSDOEDOLARAPCNOAPOUNTSTROAGNATHANGTINDTLOCLVNAQDOR
THOUTH AGGRANN THE THERGRADFTWAT KETWANIAUNTSTROAGSTAGTHD
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NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW
LQVDPQKTMKVTGVTTYOGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
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VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ
                                                                                                            /note="polyadenylation signal"
8967 €
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RLPKGVKHLKOFPILFGEIFKYKWTVTVEOGPFKSDFRCITRYSSFVNNERDLASGL
IGPLLICYKESVDQRGNOIMSDKRNYLLFSVPDENRSWYLTENIQRFLPUPAGVOLED
DEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMV
                                                              /note*"polyA site"
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KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
AVFDEGKSWHSETKNSLMQDRDAASARAWPKNHTVNGYVNRSLPGLIGCHRKSYVWHV
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110. .166
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VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa
                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTGAATTCAGGCCTCATTGGAGCCCTA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgttatcctactgga
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86081164
2 (site
                                                        Characterization of the polypeptide composition of human factor {\tt VIII:C} and the nucleotide sequence and expression of the human
                                                                                          Truett, M.A., Blacher, R.W., Burke, R.L., Caput, D., Chu, C., Dina, D., Hartog, K., Kuo, C.H., Masiarz, F.R., Merryweather, J.P., Najarian, R., Pachl, C., Potter, S.J., Puma, J., Quiroga, M., Rall, L.B., Randolph, A., Urdea, M.S., Valenzuela, P., Dahl, H.-H.M., Favalaro, J., Hansen, J., Nordfang, O. and Ezban, M.
                         kidney cDNA
DNA 4 (5), 333-349 (1985)
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9029)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                          Human kidney, cDNA to mRNA, clones pF8[100,102]; and cell line GM1416 DNA, clone pF8-4.3.
                                                                                                                                                                                                                                                                              coagulation factor VIII:C
                                                                                                                                                                                                                                                                                             M14113.1 GI:182817
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(sites)
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96.2%;
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Pred. No. 2.5e-154;
                                                                                                                                                                                                                                                                                                                                             mRNA
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[3] site
[2] site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.A.Truett, 26-FEB-1986.
The mutation at position 1042 results in a change of Glu to and the one at position 1043 in a change from Glu to Gly. T mutation at position 1042 produces a premature stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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DeRosa, V. and Marchetti, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2] sites; mutations causing hemophilia.

Draft entry and clean copy sequence for [1] kindly provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sites)
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RLPKGVKHLKDPPILPGEIFKYKWTVTFUGGPYKSDPPRCLTRYYSSFVNMERDLASGL
IGPLLICYKESVDORGNOIMSDKRNVILFSVEDENRSNYLTENIQRELPUPAGVOLED
PEFQASNIMHSINGYVFDSLOLSVCLHEVAYWYILSIGAQTDPLSVFFSGYTFKHKMV
YEDTLTILFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYED
SYEDLSAYLLSKNNALERPSFSONSHRPSTROKOFNATTIPENDIEKTDWFAHATPW
PKIQNVSSSDLLMLLROSPTPHGLSLSDLQEAKYETFSDDPSPGAIDSNNSLSEMTHF
RQQLHHSGDMVTTPESGIQLRLMEKLGTAATELKKLDFKVSSTSNNLISTIPENDIA
AGTDNTSSLGEPSMPWYDSOLDTILFGKKSSPLTESGGPLSLSEENNDSKLLESGINA
AGTDNTSSLGEPSMPWTSOSOLDTILFGKKSPBLTESGGPLSLSEENNDSKLLESGIN
NSOESSWGKNVSSTESGRLFKGKRAHGPALLTKDNALFKVSISLLKTNKTSNNSATNR
                                                                                                                                                                                                                                                  KTHIDGPSLLIENSPSVWQNILESDTEFKKVTPLIHDRNLMDKNATALRLNHMSNKTT
SSKNNEMVQOKKEGP I PPDAQNEDMSFFKMLFLESSARAVIQRTIGKNSLUSGGGFSPK
OLVSLAPEKSVEGQNELSEKNKVVVCKGEFTKDVGLKEMVFPSSRNLFEITLDDNLHEN
NTHNQEKKIQEEIEKKETLIQENVVLPQIHTVTGTKNFMKNLFLLSTRQNVEGSYDGA
YAPVLQDFRSLADSTNRFKKHTAHFSKKGEEBNLECLGNQTKQIVEKYACTTRISPNT
SQQNVTQRSKRALKOFRLPLEETELEKRIIVDDTSTQMSKNNKHLTFSTLTQLDVXH
SQQNVTQRSKRALKOFRLPLEETELEKRIIVDDTSTQMSKNNKHLTPSTLTQLDVXH
KEKGAITQSPLSDCLTRSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHLP
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IGMGTTPEVH3IFLEGHTFLVRNHRQASLEISPITFLTAGTLLMDLGGFLLFCHISSH
QHDGMEAYVKVDSCPEEDLHMKNNEEAEDVDDDLTDSEMDTVRFDDDNSPSFTQIRS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFNIAKPRPPMMGLLGPTIQAEVYDT
VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
                          FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
DYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLGPYIRA
                                                                                                                                AASYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMTGDQREVGSLGTSATNSVTYKKV
ENTVLPKPDLPKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGGSLQGTEGAI
KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQFDFA
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/protein_id="AAA52485.1"
/db_xref="GI:182818"
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172. .228'
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/db_xref="taxon:9606"
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EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F8C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MQIELSTCFFLCLLRFCFSATRRYYLGAVELSWDYMQSDLGELP/
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LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFVGNQ
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Lollar, J.S. and Runge, M.S.
Hybrid human/animal factor VIII
Patent: US 5744446-A 1 28 APR-1998;
Location/Qualifiers
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AR003710 GI:3964969
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Modified factor VIII
Patent: US 5859204 A 1 12-JAN-1999;
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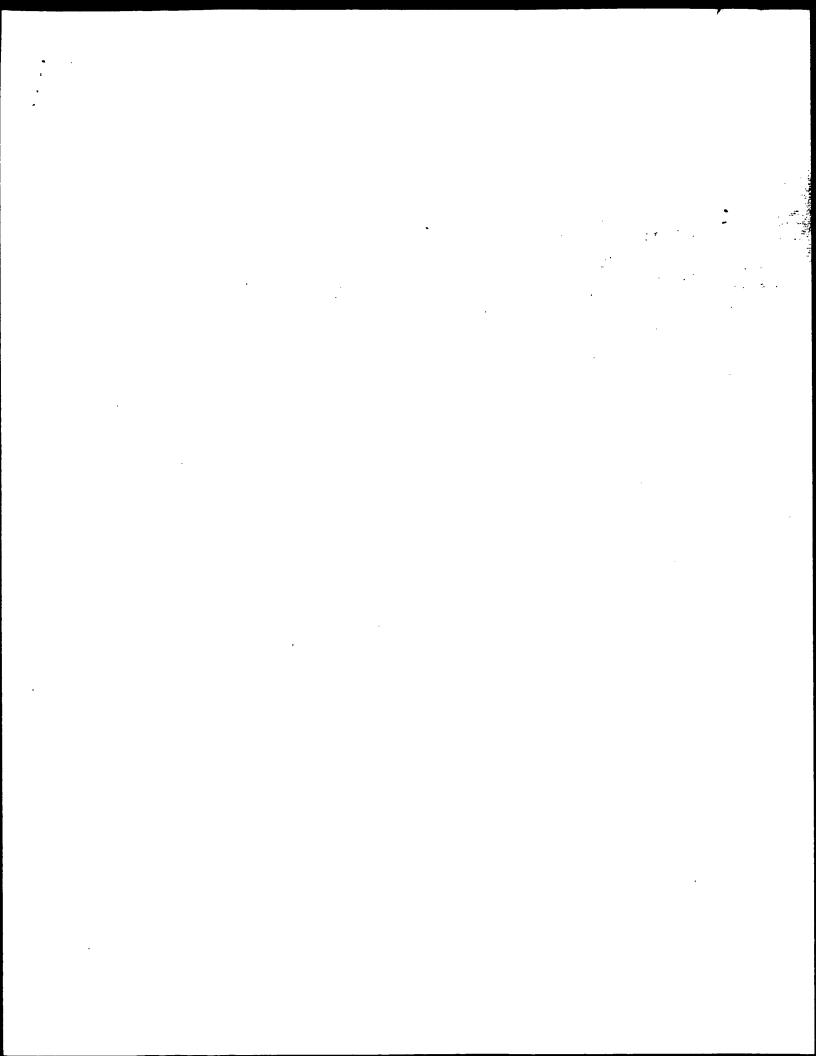
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Lollar, J.S.
Modified factor VIII
Patent: Us 6180371-A 1 30-JAN-2001;
Location/Qualifiers
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1907 c. 1844 g
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96.0%; Pred. No. 7.1e-154;
tive 0; Mismatches 25;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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41.4 41.3 41.0 40.9 40.6	42.9 42.9 41.8	45.1 44.0 43.5	45.7 45.3 45.1	46.6 46.1 45.9	48.8 48.8 47.6 46.7	0 0 0	<u>,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</u>	54.8 54.5 54.1
414 501 718 640 738	705 705 715 751	684 911 706 686	647 832 474	890 721 725	604 499 551 683	710 575 620	711 890 619	696 801 554 720
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AV404393 AV596377 AG009622 B84895 AL598454	AG004170 AG010296 AG013813 AG007414	AG014348 BG923556 AG000533 AG016243	AG008943 BG923768 AV601733	B07159 AL044583 AG001126	AG002706 AV612734 AL041936 BG838185	CNS075W1 AZ918759 AL599532	AG010947 AL046135 AV611386	BE573230 BE569687 AL041808 AG000534
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## ALIGNMENTS

RESULT

FEATURES Source		JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	BG838279/c LOCUS DEFINITION
	Eastern (ereal and Ollseo Research Centre Agriculture and Agri-food Canada Agriculture and Agri-food Canada 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KlA 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Fax: (613) 759-1701 Fax: (613) 759-1701	Unpublished (2001) Contact: Singh,J.A.	, N.A. Expressed Sequence Tags from Cold-Stressed Glycine clandestina Seedlings	1 (bases 1 to 935) 1 (bases 1 to 935) Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris ,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker	Glycine clandestina. Glycine clandestina (Glycine c	EG838279.1 GI:14204601 EST.	BG838279 935 bp mRNA EST 25-MAY-2001 GC01_10e07_R GC01_AAFC_ECORC_cold_stressed_Glycine_clandestina Glycine clandestina cDNA clone Gc01_10e07, mRNA sequence.

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                                                                       TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAA
                                                                                          tatttagaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctga 779
                                                                                                                                                       TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Leaves, stem"
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98,5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp434Ell1) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone Insert
Clone from S. Wiemann, Molecular Genome Analysis, German Can-
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +49-30-84131623
Fax: +49-30-84131128
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DKFZp434E111_r1 434 (synonym: h

DKFZp434E111 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No s1 sequence available.
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Innestrasse 73, 14195 Berlin, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Poustka A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poustka, A., Klein, M., Mewes, H.W.,
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1 (bases 1 to 841)
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/dev_stage="adult"
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/clone_lib="434 (synonym: htes3)"
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/db_xref="taxon:9606"
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BG920379.1 GI:14300855
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                                                                                                                                                                                                High quality sequence start: 15 High quality sequence stop: 717.
                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln#.gov
                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                  LLAM10916
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                       /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue-yepe="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                 /clone="IMAGE:4954975"
                                                                                                                                /db_xref="taxon:10090"
                                                                                                                                            /strain="FVB/N"
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                                                                 ALO40542 767 bp mRNA
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DKFZP434I1114 5', mRNA sequence.
ALO40542
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671 gaagcatttatcagggttattgtctcatgagcggatacatatttgaatgtatttagaaaa 730
                                                         611 agggaataagggcgacacggaaatgttgaatactcatactcttccttttttcaatattatt 670
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                                                                                                                                                                                                                                                         GAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCT 406
                                      AGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATT 226
                                                                                                                                                                                  TACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCAT 346
                                                                                                                                                                                                   taccgctgttgagatccagftcgatgtaacccactcgtgcacccaactgatcttcagcat 550
                                                                                                                                                                                                                                                                                                                                                                                                                           ccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaatagtgta 370
                                                                                                                                                                                                                                                                            gaactttaamagtgctcatcattggaaaacgttcttcggggcgaaaactctcaaaggatct 490
                                                                                                                                                                                                                                                                                                                                                                                                      CCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgcagtgttatcactcatggttatggcagcactgcataattctctttactgtcatgccat 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin-Charlottenburg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
158 c 168 g 221 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKFZp43411114"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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Best Local Similarity
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602 ccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcctttttc
                                                          505 CTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATG
                                                                                                                                          565 CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGAT
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                                                                                  542 cttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatg
                                                                                                                                                               482 caaggatettaecgetgttgagatecagttegatgtaacecaattegtgcacecaactgat 541
                                                                                                                                                                                                                        625 CACATAGCAGANCTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT
                                                                                                                                                                                                                                               422 cacatagcagaactttaaaagtgctcatcattggaaaacgttcttcgggggggaaaactct 481
                                                                                                                                                                                                                                                                                                      685 AATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGNATAATACCGCGC
                                                                                                                                                                                                                                                                                                                           362 aatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccggcgc 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Qiaqen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No s1 sequence available. This clone (DKFZp31301920) is available at the RZPD in Berlin
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Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consortium of the German Genome Project.
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfIIB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone~"DKFZp31301920"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 638; DB 10;
Pred. No. 1.9e-172;
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Matches 639;
                                    Query Match
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                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCCGTCAGGGCGCGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL042640 688 bp mRNA EST 29-FEB-2000 DKFZp434M0421_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0421 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82752 Martinsried, Germany
Am Klopferspitz 18a D-82752 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. Wiemann@dkfz heidelberg.de;
sequenced by LMU (Ludwig Maximilians University
Sequenced by LMU (Ludwig Maximilians University
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Blum H
                                                                                                                                                                                                                                                                                                                     Berlin-Charlottenburg, GERMANY; Email: iocațion/Qualifiers
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                                                                                                                          190
  Conservative
                                                                                                                                                                             /clone_lib="434 (synonym:
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                        /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
150 c 158 g 190 t
                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                          /clone="DKFZp434M0421"
                       63.6%;
      0;
                         Pred. No. 4.7e-172;
                                             Score 636.6;
        Mismatches
                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                   clone@rzpd.de
          Indels
                                                 Length 688;
          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Locus
                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 tctgtgactggtgagtactcaaccaagtcattctgagaatagtgtatgcggcgaccgagt 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685 gyttattytotoatgagoggatacatatttgaatgtatttagaaaataaaacaaataggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745 gttccgcgcacatttccccgaaaagtgccacctgacgtctaag 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACGGAAATGTTGAATACTCATACTCTTTCCTTTTTCAATATTATTGAAGCATTTATCAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCCGCAAAAAAGGGAATAAGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcatcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgaga 504
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                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1. (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                                                                             BE569261 914 bp mRNA
601331179F1 NCI_CGAP_Mam6 Mus
                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM8928 row: m column: 20
                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                          BE569261.1 GI:9812981
                                                                                                                                                                                                                                                                                                                        house mouse
                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
quality sequence stop: 685
                                                                                                                                                                                                                                                                                                                                                                                                                 musculus cDNA clone IMAGE: 3708859 5'
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                                                                                                                                 601 TTTTCCCCGAAAAGTGCCACCTAAATGGTAAG
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                                                                                                                                                                                                                                                                                 637 tgaatactcatactcttctttttcaattattgaagcatttatcagggttattgtctc 696
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                                                                                                                                                                                              ATGAGCGGATACATATTTGAATGTATTAAGAAAAATAAACAAATAGGGGTTCCGCGCACA
                                                                                                                                                                                                                  atgagcggatacatatttgaatgtatttagaaaaataaaacaaataggggttccgcgcaca 756
                                                                                                                                                                                                                                                                  TGAATACTCATACTCTTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTC
                                                                                                                                                                                                                                                                                                                                       TGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAAGGGAATAAGGGCGACACGGAAATGT 480
                                                                                                                                                                                                                                                                                                                                                         tgagcaaaaacaggaaggcaaaatgcògcaaaaaagggaataagggcgacacggaaatgt 636
                                                                                                                                                                                                                                                                                                                                                                                                           TAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                        taacccactcgtgcacccaactgatcttcagcatcttttactttcaccagcgtttctggg 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATG 360
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AL042540 702 bp mRNA EST 29-FEB-2000 DKFZP434I1621_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434I1621 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH*

a 207 c 199 g 233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3708859"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.7%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.4e-163;
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TITLE
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281 AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGC
                        546 agcatcttttactttcaccagcgtttctgggtgagcaaaaacagggaaggcaaaatgccgc 605
                                                                                          341 GATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
                                                                                                                                                                                  401 TAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 CCATGTTGTGCAAAAAAGCCGGTTAGCTCNTTCGGTCCTCCGATCGGTTGTCAGAAGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ccatgttgtgcaaaaaagcggttagctccttcggtcctccgatc-gttgtcagaagtaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 GTATGGGCTTCCATTCAAGCTCCCGGTTCCCCAACGATCAAGGCGAAGTTACATGATCCC 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 gtttggtatggcttcattcagctccggttcccaacgatcaaggcg-agttacatgatccc 187
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                                                                                                                                                                                                                                                                             GTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACA
                                                                                                                                                                                                                                                                                                        9t9tat9c9gcgaccga9tt9ctctt9ccc9gcgtcaatacg9gataatacc9cgccaca 425
                                                                                                                                                                                                                                                                                                                                                                                                  gccatcogtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaata 365
                                                                                                                       9atcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactgatcttc
                                                                                                                                                                                                             tagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactctcaag
                                                                                                                                                                                                                                                                                                                                                                       GCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCAATAATTCTCTTACTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No s1 sequence available.
This clone (DRFZp434I1621) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubherweg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin-Charlottenburg, GERMAN Location/Qualifiers
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This is the 5' sequence of the clone insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
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/lab_host="DH10B"
/note="Vector: pSport1;
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
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96.2%;
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Pred. No. 4.7e-159;
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515 CCATGTTGTGCAAAAAGCGGTTAGCCTCTTCGGTCCTCCGATCGTTGTCAG-AGTAAGTT 457
             69
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                                                                            gtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttacatgatcccc 188
                                                                                                          AGTTAATAGTTTGCGCAACGTTGTTGCCAATGCTACAGGCATCGTGGTGTCACGCTCGTC 576
                                                                                                                         agttaatagtttgcg@aacgttgttgccattgctacaggcatcgtggtgtcaccgctcgtc 128
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
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Hattori,M., Ishii,K., Shiba,T. and Sa
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                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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AG014918
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Masahira Hattori, Kitasato University, Department of Science,
Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens genomic DNA,
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Hattori, M., Ishii, K., Toyoda, A., Shiba, T. &
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998) In press
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.3e-155;
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Hattori,M., Ishii,K., Shiba,T. and Sakaki,
Homo sapiens ganomic DNA, chromosome 21q
Published Only in DataBase (1997) In press
                                                                                                                                                                                        Submitted (31-CCT-1997) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Labbratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
                                                                                                                                                                                                                                                                    Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)
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185 c
                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Submitted (06-JUL-1998) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, Kitasato University, Department of Science Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Jap.
                                                       Published Only in DataBase (1998) In press (2008es 1 to 696)
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                     survey sequence.
AG009765 AG003576
AG009765.1 GI:328
                                                                                                                    Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y. Homo sapiens genomic DNA, chromosome 21g
                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 696)
                                                                                                                                                                                     Eukaryota;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 696)
                                                                                                               BE573230 696 bp mRNA
601333125F2 NCI_CGAP_Mam6 Mu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
Fax:0427-78-9561)
On Feb 5. 1999 this sequence version replaced gi:2706702
AG003576: Submitted (19-Dec-1997).
                                                                                       mRNA sequence.
BE573230
                                     Mus musculus
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                                                                            BE573230.1 GI:9816950
                                                    nouse mouse.
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/clone="P8G4SpN15"
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/db_xref="taxon:9606"
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Pred. No. 2.6e-148;
0; Mismatches 0;
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AAATGTTGAATACTCATACTCTTTCCTTTTTCAATATTA-TGAAGCATTTATCAGGGTTA-
                    TCTGGGTGAGCAAAAACAGGAAGGCAAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGG
                                                                                           tctgggtgagcaaaaacaggaaggcaaaatgccgcaaaaaagggaataagggcgacacgg 630
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM8933 row: a column:
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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a 157 c 152 g 191 t
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/db_xref="taxon:10090"
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             ccgatcgttgtcagaagtaagttggccgcagtgttatcactcatggttatggcagcactg
                                        TCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert St
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 801)
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601332450F1 NCI_CGAP_Mam6
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Plate: LLAW8931 row: d column:
High quality sequence stop: 615.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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milarity 94.3%;
Conservative
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                                                                                                                                                                                                                                                                                  providing samples: Jeffrey Green, M.D., NIH<sup>*</sup>
194 c 177 g 217 t
                                                                                                                                                                                                                                                                                                            Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary; Vector: pCMV-SPORT6;
Site_2: NotI; Cloned unidirectionally. Prim
                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/clone="IMAGE:3709789"
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                                                                                   Please contact the
                                                                                                                                                                                                                                                                                                                                          human
 /clone="DKFZp434B0518"
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598 TACTCCATACTCTTCCTTTTCAAGTATTTATCGAAGCATTTCATCAGGCTTATGGTCTC
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                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL041808 554 bp mRNA EST 29-FEB-2000 DKFZp434B0518_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0518 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 554)
                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                This clone (DKFZp434B0518) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ottenwaelder B
                                                                                Berlin- Charlottenburg, GERMANY; Email:
    Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                       Ressourcenzentrum, Heubnerweg
                                                                                                              clone@rzpd.de
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Best Local Similarity 99.3
Matches 548; Conservative
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Local Similarity 99.3%;
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                                                                                                                        tcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatgtaacccact
                                                       aaagtgccacct 777
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                                                                                              tacatatttgaatgtatttagaaaataaacaaataggggttccgcgcacatttccccga 765
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                                               AAAGTGCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="UH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
a 123 c 124 g 155 t
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         8, 2002,
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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1: /SIDS2/gcgdata,
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Listing first 45 summaries
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// SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT: *
// SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT: *
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1999.219 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query		•		
No.	Score	Match	Match Length DB ID	DB·	ID	pescription
1	1000	100.0	4999	21	AAD00122	Recombinant adeno
2	1000	100.0	4999	22	AAD08613	Human factor VIII
w	736.2	73.6	11933	21	'AAD00121	Recombinant adeno
4	736.2	73.6	11933	22	AAD08612	Human tactor VIII
տ	640	64.0	7944	22	AAF84647	Plasmid DLZb encod
σ	593.2	59.3	12445	21	AAA49232	Vector HSQReneo ic
7	592.2	59.2	5035	18	AAT69811	Factor VIII-d8695-
8	590.6	59.1	4832	19	AAV19581	Human Tactor VIII
9	590.6	59.1	4832	19	AAV15338	Human Factor VIII
10	590.6	59.1	8967	17	AAT31031	Factor-Attriutti
11	590.6	59.1	8967	22	AAC87526	Human Tactor VIII

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AAF84648	AAV12112	AAV23339	AAN80444	AAN90654	AAN80446	AAN80447	AAX82258	AAN50375	AAT73164	AAQ76016	AAX88293	AAQ66615	AAA49231	AAN81544	AAN60689	AAT51357	AAV18884	AAN81096	AAN81439	AAT03571	AAX82260	AAX82261	AAX82259	AAC90508	AAX91162	AAV25810	AAT61548	AAQ50185	AAV19580	AAV15359	AAF60309	AAZ38604	AAN50054
Plasmid DLZ/ encod	prens			С	MODIFIED FACTOR AT		=	DNA sequence encou		B-domain dereted r	Human ractor viii	Sequence of fidulati	DNA CONSCIUCT HOSE	Human Factor VIII	Sequence encouring	Factor VIII:C codi	Homo sapiens ideio		Factor VIII CUNA 1	Factor-Vill CUNA.					Human factor VIII		$\sim$	Human Factor VIII					Human factor VIII

## ALIGNMENTS

RESULT AAD00122

AAD00122 standard; DNA; 4999 BP

AAD00122;

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20-OCT-1998;
24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                        Recombinant Adeno Associated Vector; rAAV; pVm4.1cF8deltaB; promoter; human Factor VIII; hFVIII; EF1alpha; human elongation factor-lalpha; human growth hormone; hGH; ITR; inverted terminal repeat; haemophilia;
                                                                                                                                                                                                                                                                                                              31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                      Recombinant adeno associated vector construct, pVm4.1cF8deltaB.
                                                                                                                                                              27-APR-2000.
                                                                                                                                                                                                          Adeno associated virus.
                                                                                                                                                                                                                                gene therapy; ds.
New recombinant adenovirus-associated vector, useful for gene therapy
                                              Couto LB,
                                                                                                                                      19-0CT-1999;
                                                                                                                                                                                   WO200023116-A1
                      WPI; 2000-339536/29.
                                                                    (AVIG-) AVIGEN INC.
                                              Colosi PC;
                                                                                           98US-0104994.
99US-0125974.
99US-0364862.
                                                                                                                                        99WO-US24495
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to treat hemophilia, comprises at least a operably linked to control sequence -
9; Fig 6; 92pp; English.
                                                                                      portion of Factor VIII
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The present DNA sequence is a recombinant adenovirus-associated vector, CC (rAAV) construct pVm4.1cP8deitaB. This expression vector comprises the CC promoter, first intron (-573 to +985) of human elongation factor-lalpha CC (EFlalpha) gene, human Factor VIII coding sequence (hGH). This sequence is CC inserted between the AAV inverted terminal repeat (ITR) regions. The CC inserted between the AAV inverted terminal repeat (ITR) regions. The CC first 57 bp encoding the 19 amino acid signal peptide, Al and A2 domains CC and 5 amino acids from the N-terminus of the B domain. The light chain CC segment comprises the C-terminus of the B domain and the A3, CC land C2 domains. Both the heavy and light chain segments are cloned control sequences, that directs the transcription and translation of the CC control sequences, that directs the transcription and translation of the CC factor VIII gene. The adeno-associated viral vectors are used for gene conficency, because of their broad host range, safety profile and duration in the inferted hosts.

Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;

DB 21;

Length 4999;

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suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a

The present invention relates to a method for treating a subject

second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector i useful in gene therapy for treating haemophilia A in mammals, in

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                                                                                                                  Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood coagulation factor VIII \,
                                                                                                                                                                                        Couto LB,
                                                                                                                                                                                                                                                                                                                              Chimeric - Adeno associated Chimeric - Homo sapiens. Chimeric - Unidentified.
                                                                                                                                                                                                              (AVIG-) AVIGEN INC
                                                                                                                                                                                                                                     22-DEC-1999;
                                                                                                                                                                                                                                                          21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                                                       Human factor VIII expressing rAAV vector pVm4.1cF8-B partial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD08613 standard; DNA; 4999
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                                                                                                                                                                                                                                                                                                                                                                             pVm4.1cF8-B;
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Sequence 11933 BP; 3258 A; 2818 C; 2717

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3140 T; 0 other

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                                                             hrVIII coding region comprises the heavy chain gene segment with the first 57 bp encoding the 19 amino acid signal peptide, Al and A2 domains and 5 amino acids from the N-terminus of the B domain. The light chain segment comprises the C-terminal 85 amino acids of B domain and the A3, segment comprises the C-terminal 85 amino acids of B domain and the A3, cl and C2 domains. Both the heavy and light chain segments are cloned into the same plasmid seperated by 42 nucleotides coding for 14 residues of the B domain, that is deleted. This plasmid is operably linked to control sequences, that directs the transcription and translation of the Factor VIII gene. The adeno-associated viral vectors are used for gene therapy to treat haemophilia. This method allows prolonged expression of therapy, because of their broad host range, safety profile and duration of expression in the infected hosts.
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24-MAR-1999;
30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant adeno associated vector construct, pAAV-F8-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF 3 albumin promoter, the first intron (-573 to +985) of human elongation factor-lalpha (perlalpha) gene, human Factor VIII coding sequence (hFVIII) and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The
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                                                                                                                                                                                                                                               CC The present invention relates to a method for treating a subject CC suffering from a blood clotting disorder. The method comprises CC administering a recombinant adeno-associated virion (rAAV) comprising CC a nucleotide sequence encoding the light chain of factor VIII and a CC second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is cuseful in gene therapy for treating haemophilia A in mammals, in CC particular humans. The rAAV vector provides high level and long term cappersion of biologically active clotting factor VIII in vivo. The present sequence is pAAV-F8-1 vector without the plasmid backbone. It comprises HNF-3.mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EFlalpha) and immunoglobulin GC LigG) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the collish and heavy chains of human factor VIII.
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Best Local Similarity
                                                                                                                                 Matches 870;
                                                                                                                                                                                                               Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating blood clotting disorder, especially hemophilia in mammals, administering recombinant adeno-associated vectors which express bloosgulation factor {\tt VIII}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Fig 5; 90pp; English.
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Chimeric - Oryctolagus cuniculus.
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Adeno-association disorder; ss.
                                                                                                                                              AAF84647 standard; DNA; 7944 BP.
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                               Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
                                                            Plasmid DLZ6 encoding human B-domain deleted factor VIII.
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                                                                                                                                                                                                                                                                      vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one enhancer and at least one promoter. The method results in the production of high titer rAAV vector stocks carrying the B-domain deleted factor VIII transgenes and expression cassettes, which generate adequate titers of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded B-domain deleted factor VIII, which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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P-PSDB; AAB67959.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression control element -
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                                                                                                                                                                                                                                               Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
                136 aggggttcctgcggcgcacgcgtggt-ggcgcggggtaaactggggaaagtgatgtcgtg
   135
                                                                                                                15 ctgcgcgctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggcttt 74
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nes 785; Conserv
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aggggttcctcagatctctttctaagtaaacagtacatgaacctttaccccgttgctcgg
                                                        gcccgggcgcctcagtgagcgagcgagcgcagagagggagtggccaactccatcact
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/note= "TK polyA sequence"
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/note= "human B-domain deleted factor VIII"
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/note= "hepatitis B virus EnhI enhancer"
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               Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; vector; osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract; haemophilia;
      Factor VIII; human; transgene;
                                                                                                                                                                                                                                                      AAA49232 standard; DNA; 12445
                                                                                                                                                                    26-SEP-2000 (first entry)
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The invention relates to a method for expanding the population of CC endothelial cells (EC) obtained from peripheral blood, by culturing, CC in contact with a collagen I coated surface, buffy coat cells obtained CC from peripheral mammalian blood in the presence of a culture medium CC containing vascular endothelial growth factor (VEGF) and free of bovine brain extract. EC are useful for treating hemophilia by introducing it CC into the blood stream of a mammal, so that an effective amount of CC fractor VIII protein is secreted in the blood stream of the mammal. CC will gene into which an enhanced green fluorescent protein coding CC sequence (HSQ) has been inserted, is subcloned. Transgenic EC transduced in vitro are useful for improving prosthetic implants. EC is also useful for diagnosing clotting disorders where indication or disease is CC associated with a reduction in the activity of an enzyme. EC is also useful in gene therapy for treating the variety of diseases including adenosine deamninase deficiency, sixkle cell anemia, thalassemia, then activity of an enzyme activity of such as Alzheimer's disease, heart diseases, defects in immune system, for reactive benefit and transfers.
Sequence 12445 BP; 3255 A; 2989 C; 2951 G; 3250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with collagen I coated surface in culture medium comprising vascular endothelial growth factor -
                                   for repairing bone fractures and to treat or prevent osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Fig 4; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-412303/35
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(UYEM-) UNIV EMORY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sickle cell anaemia; thalassemia; diabetes; alpha-antitrypsin deficiency; Alzheimer's disease; brain disease; heart disease; immune system defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fracture; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEBBEL R P
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Best Local
           559 atttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtacaaaaagac
                                       851 agtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtggacgcaag
                                                                                                             791
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                                                         agtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgggacgcaag
                                                                                                    cttctttctgtgccttttgcgattctgctttagtgccaccagaagatactacctgggtgc
                                                                                                                    cttctttctgtgccttttgcgattctgctttagtgccaccagaagatactacctgggtgc
                                                                                                                                                               tccgcatcgaccggatcggaaaacctctcgagccaccatgcaaatagagctctccacctg
                                                                                                                                                                                tocactttttcttttttctccacaggtatcgatccaccatgcaaatagagctctccacctg 438
604;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                             59.3%;
97.1%;
                                                                                                                                                                                                                                             Score 593.2; DB 21
Pred. No. 8.6e-162;
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                           DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT69811 standard; DNA; $5035 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1331 ttcaggcctcattggagcccta 1352
                                                                                                                                                                                                                                                                                                                                                                                                                     Factor VIII-db695-HCII; heparin cofactor II; blood coagulation; blood clotting; procoagulant; anticoagulant; antithrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor VIII-dB695-HCII DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 atttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtacaaaaagac
                                                                                                                                                                                                                                                                                                                                                                                                         haemophilia; gene therapy; ss..
                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
donor anticoagulant \Phi_{P} r antithrombotic protein of coagulation disorders
                   Hybrid Factor VIII with modified activity, comprises region from donor anticoagulanton antithrombotic protein - useful for treats
                                                                                                                                                                                  13-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   979 ttcaggcctcattggagcccta 1000
                                                      P-PSDB; AAW18670.
                                                                                                                         (IMMO ) IMMUNO
                                                                                                Voorberg JJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaatggcctc
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                                                                     1997-289291/26.
                                                                                                                                                       95US-0558107
                                                                                                                                                                                  96WO-EP04977
                                                                                                                                                                                                                                                                                           /product= Factor VIII-dB695-HCII
2225..2314
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 35..5020
                                                                                                                                                                                                                                                             /product= heparin cofactor II region (aa51-81)
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                    for treatment
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RESULT AAV19581

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AAV19581 standard; cDNA; 4832

AAV19581;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA molecule (AAT69811) codes for Factor VIII-dB695-HCII (AAW18670), a hybrid protein in which amino acids 712-736 of Factor-dB695 (Factor VIII de1868-1562) B-domain are replaced by amino acids 51-80 from the acidic region (and potential thrombin-binding site) of human heparin cofactor II (HCII). It was obtd. by PCR amplification (see also AAT69812-13) of the HCII acidic region from total liver cDNA, fusion to sequences encoding Factor VIII total liver cDNA, fusion to sequences encoding Factor VIII aa706-711 and aa737-743, and incorporation of the construct into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid pCLB-dB695. The hybrid protein, which can be expressed using gene therapy techniques, has increased procoagulant activity owing to the HCII acidic region, and can be used to treat blood coagulation disorders such as haemophilia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 52-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5035 BP; 1484 A; 1127 C; 1110 G; 1314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 aggtcctaccatccaggctgaggtttatgatacagtggtcattacacttaagaacatggc 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 agaaltcacggatcaccttttcaacatcgctaagccaaggccaccctggatgggtctgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 tagagtgccaaaatcttttccattcaacacctcagtcgtgtacaaaaagactctgtttgt
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 607
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                     cattggagcccta 1000
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                                                                     gtgccttacctactcatatctttctcatgtggacctggtaaaagacttgaattcaggcct
                                                                                                                                                                aagccatacatatytctggcaggtcctgaaagagaatggtccaatggcctctgacccact
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                                                                                      gtgccttacctactcatatctttctcatgtggacctggtaaaagacttgaattcaggcct
cattggagcccta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                    606
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06-AUG-1998

(first entry)

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intravenously to a human. The long term systemic expression results in a comeasurable level of the therapeutic protein being produced in the blood cof the human for a period of at least 30 days after the administration of the RRV vector preparation. RRV's can be used for in vivo delivery of therapeutic protein to treat, e.g. haemophilia A, haemophilia B, cycler such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, combined immunodeficiency (SCID), cystic fibrosis, Duchenne's evere combined immunodeficiency (SCID), cystic fibrosis, Duchenne's constitutypsin deficiency, adenine deaminase deficiency, alpha1-contitutypsin deficiency, Guacher's syndrome, anaemia, infections such as contitutypsin deficiency, Guacher's syndrome, anaemia, infections such as contituty disease or graft versus host disease, RRV's are capable of curviving inactivation in human serum thereby allowing efficient gene considered periods of time.
                                                                  Matches
                                                                                                                                                      Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA encodes the beta-domain deleted SQN deletion protein of human factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV)
            372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 28; Pages 210-213; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatitis; thalassemia; phenylketonurla; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Guacher's syndrome; high blood pressure; Alzheimer's disease, autoimmune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New replication defective recombinant retro-viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1997;
03-JUL-1996;
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                                                                                       Local
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                                                                605;
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                                                                                   Similarity
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0869309.
96US-0645601.
96US-0696381.
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Depolonj, Greengard J, Hsu DC,
R, Mittelstaedt DM, Prussak CE,
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                                                                                 59.1%;
96.2%;
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                                                              0,
                                                                           Score 590.6; DB 19
Pred. No. 3.2e-161;
                                                          Mismatches
                                                                                                DB 19;
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Indels
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        04-JUN-1997;
03-JUL-1996;
13-AUG-1996;
                                                               02-JUL-1997;
                                                                                                                                                        CDS
                                                                                       08-JAN-1998
                                                                                                                W09800542-A2
                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                retrovirus; vector;
                                                                                                                                                                                                                                      Factor VIII; blood clotting; haemophilia A; gene therapy;
                                                                                                                                                                                                                                                                    Human Factor VIII SQN deletion mutant DNA.
                                                                                                                                                                                                                                                                                                 20-JUL-1998
                                                                                                                                                                                                                                                                                                                                               AAV15338 standard; DNA; 4832 BP
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                        97US-0869309
96US-0645601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA sequence includes a coding region for the B domain deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-743 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 and A3 Factor VIII domains. When compared to plasmid-derived and A3 Factor VIII domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New replication defective recombinant retroviruses: - which express domain-deleted human factor VIII or human factor IX for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4832 BP; 1381 Av 1089 C; 1055 G; 1307 T; 0 other;
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                 852 aagtottocotggtggaagccatacatatgtotggcaggtootgaaagagaatggtocaa 911
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aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa
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Mittelstaedt DM,
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96.2%;
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NJ, Greengard J, H
t DM, Prussak CE,
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Matches

605;

Conservative

372 actgacatccactttttctttttctccaccaggtatcgatccaccatgcaaatagagctct 431

66 attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125

Query Match Best Local Similarity

59.1%; 96.2%;

Score 590.6; Pred. No. 4.

.6; DB 17; 4.2e-161;

Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Factor-VIII full-length cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                      W09621035-A2
                        transduce cells either in vivo or ex vivo. Factor-VIII expressed from such transduced cells will be processed and transported in a fashion analagous to the expression product of a normal Factor-VIII gene. Retroviral particles harbouring such vectors will be useful in the gene therapy of haemophilia A.
                                                                                                                                                                                                                                                                                                                                       30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1995;
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Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                          packaged into infectious retroviral particles. These may be used
                                                                                                        (AAW00465), a trace plasma glycoprotein which acts as a cofactor in conjunction with Factor-IXa in the activation of Factor-X. Retroviral vectors comprising the full-length contact be efficiently
                                                                                                                                             A full-length cDNA clone (AAT31031) codes for human Factor VIII
                                                                                                                                                                           Claim 3; Page 58-68; 86pp; English.
                                                                                                                                                                                                  Retroviral vector directing expression of full length factor VIII used in the gene therapy and treatment of haemophilia A
                                                                                                                                                                                                                                            P-PSDB; AAW00465
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                    WPI; 2001-025163/03.
                                            Saenko EL,
                                                                                            24-MAY-1999;
                                                                                                                  24-MAY-2000; 2000WO-US14111
                                                                   (AMNA-) AMERICAN NAT RED CROSS
                                                                                                                                                                  WO200071714-A2
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                Factor VIII; human; A2 domain; C2 domain; LRP-mediated plasma clearance;
                                                                                                                                                                                                                                                             Human factor VIII cDNA, SEQ ID NO:1.
                                                                                                                                                                                                                                                                                        13-MAR-2001
                                                                                                                                                                                                             receptor-dependent clearance; receptor-independent clearance; haemophilia; half-life; ss.
                                                                                                                                                                                                                                                                                                                                     AAC87526 standard; DNA; 8967
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in the bloodstream. The A2 domain mutants exhibit reduced LRP-dependent (receptor-dependent) clearance of factor VIII, while C2 domain mutants have reduced LRP-dependent clearance. The invention also relates to a method of using RAP (receptor associated protein), a protein which inhibits LRP (low density lipoprotein related protein)-mediated ligand internalisation, to increase the half-life of factor VIII. The mutant factor VIII proteins, and nucleotides encoding them, are useful for treating haemophilia. RAP, LRP-binding RAP mutants or fragments, and nucleic acids encoding them may also be used in the treatment of haemophilia, in combination with a mutant factor VIII protein or DNA of the invention. The invention provides means of increasing the half-life of factor VIII by reducing its clearance from plasma. The present sequence represents cDNA encoding human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid substitution at one or more positions in the C2 domain. The invention also encompasses a factor VIII mutant which lacks a B domain (AAB48842). The factor VIII mutants have an increased half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human factor VIII mutants comprising an amin acid substitution at one or more positions in the A2 domain and/or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 41; Page 86-101; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or C2 domain of factor VIII -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor VIII mutants having increased half-life useful for treating hemophilia, comprise one or more amino acid substitutions in the {\tt A2}
8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
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Sequence

DЬ γΩ Ъ 29 В 20 В δÃ Db δÃ DЬ δÃ g QУ Ър δÃ Вp δÃ рь Š Matches Query Match 426 186 432 ccacctgcttctttctgtgccttttgcgattctgcttttagtgccaccagaagatactacc 491 246 372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431 66 Local aagtetteeetggtggaageeataeatatgtetggeaggteetgaaagagaatggteeaa tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag aagtottccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta cacttaagaacatggcttcccatcctgtcagtcttcatgctgtttggtgtatcctactgga cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg ccacctgcttcttctgtgccttttgcgattctgctttagtgccaccagaagatactacc acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125 605; Similarity Conservative 59.1%; 0, Score 590.6; DB Pred. No. 4.2e-16 Mismatches .2e-161; 22; Indels Length 8967; 0,. Gaps 665 971 605 545 485 425 671 185 365 0

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666 acttgaattcaggcctcattggagcccta 694

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Best Local Similarity
Matches 605; Conserv
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AAN50054 standard; DNA; 8975 BP.
                                                                                                                                                                                                                                                                      The gene encodes human factor VIII. The factor VII is produced in pure form and in useful amts. using recombinant DNA technology. Factor VIII can be used to correct factor VIII deficient plasma, and activates factor xt oxa in the presence of factor IXa, Ca and phospholipid. These to activities are inactivated by antibodies specific for factor VIII. The activity of the prod. is bound to an specific monoclonal antibody specific for factor VIII. Factor VIII activity is activated by thrombin. The activity is bound to, and can be eluted from, immobilised von Willebrand factor. Dose of factor VIII is 20-40 units/kg over 8 hours i.v. for maintenance therapy for haemophilia, 40 units/kg for preoperative conditions, or 15-20 units/kg for minor haemorrhaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human factor VIII gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human factor VIII; ss cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant functional human factor VIII or deriv. - useful for treating haemophilia and obtd. as pure prod. by recombinant DNA \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig. 10A(I)-10C(III); 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-PSDB; AAP50059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1984;
                                                                                                                                                                                                                                               sequence 8975 BP; 2849 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                                                                 372 actgacatccactttttctttttttctccaccaggtatcgatccaccatgcaaatagagctct 431
 186
                                                                                                             66 attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1985-277976/45.
                                                      tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg 551
tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
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                                                                                                                                                                                       59.18;
96.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawn RM, Wood WI;
                                                                                                                                                                        0 Mismatches
                                                                                                                                                                                         Score 590.6; DB 6; Length 8975; Pred. No. 4.2e-161;
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                                                                                                                   AAZ38604 standard; cDNA; 8975 BP.
                                                                                                                                                                                                                                                                                                                     non-functional; bleeding disorder; coagulation; treatment; ds
                                                                                                                                                                                                                                                                                                                               Factor VIII; haemophilia; proteolysis; heavy chain; light chain; secretion; von Willebrand Factor; vWF; C2 domain; intron 22; inv
                                                                                                                                                                                                                                                                                                                                                                 Human full-length factor VIII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         852 aagtottocotggtggaagccatacatatgtotggcaggtcotgaaagagaaatggtocaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672 cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta 731
                                                                                                                                                                                                                          signal_peptide
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972 acttgaattcaggcctcattggagcccta 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                                              W09959622-Al
                                                                                                                               polyA_signal
(GETH ) GENENTECH INC
                         20-MAY-1998;
                                               17-MAY-1999;
                                                                      25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagtottocotggtggaagocatacatatgtotggcaggtootgaaagagaatggtocaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                          98US-0082000.
                                                99WO-US10872
                                                                                                                              /product= "8948..8953
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167..5233
                                                                                                                                                                  /product= "Maximum-length human factor VIII heavy chain" 5234..7162
                                                                                                                                                                                                                            110..166
                                                                                                                                                                                                                                      /product= "Human full-length factor VIII"
                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                             "Human factor VIII light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC known binding sites at the N-terminus and within the C2 domain.

CC Haemophilia A is frequently caused by an intron 22 inversion in the C2 decoming inverted and localised telomeric to two sections, exons 1-22 becoming inverted and localised telomeric to the original site, while C2 exons 23-26 remain isolated at the original site. Exons 23-26 a portion on functional. The factor VIII gene product of individuals with this C2 mutation thus comprises domains, without which factor VIII is comproteolysis is non-functional, resulting in a bleeding disorder. The C3 invention relates to a novel method for for treating haemophilia A in a cadministering to the mammal either an effective amount of factor VIII gene encoding it, and may be useful for treating patients such as those whose haemophilia A is caused by intron 22 cinversion. The recombinant factor VIII products of this invention are creduces the risk of pathogenic infection which was previously a problem can using domated plasma. Furthermore, the invention provides a more can seed of providing factor VIII activity to patients who can are at risk of producing antibodies against full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents cDNA encoding the full-length human factor VIII. In this form, the protein is 300 kD in size with the domain structure Al-A2-B-A3-C1-C2. However, prior to secretion, this 300 kD protein is proteolysed into a heavy chain (Al-A2-B, with continued proteolysis within the B domain resulting in molecules of varying length) and a light chain (A3-C1-C2) that remains non-covalently attached to the heavy chain. Upon secretion, factor VIII is rapidly cleared from the circulation unless it is bound by the plasma protein von Willebrand Factor (VWF). Factor VIII binds to VWF through the light chain, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8975
                        672 cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                                                    306 aaaagactctgtttgtagaattcacggatcaccttttcaaccatcgctaagccaaggccac 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method for treating hemophilia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                                                                               aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac 671
                                                                                                                                                                    acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca
                                                                                                                                                                                            acgcaagatttcctcctagagtýccaaaatcttttccattcaacacctcagtcgtgtaca 611
                                                                                                                                                                                                                                                        tgggtgcagtggaactgt&atgggactatatgcaaagtgatctcggtgagctgcctgtgg 245
                                                                                                                                                                                                                                                                                 t999t9cagt9gaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg 551
                                                                                                                                                                                                                                                                                                                                                                   ccacctgcttctttctgtgccttttgcgattctgcttttagtgccaccagaagatactacc 491
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 590.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 4.2e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 8975;
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                                                       The present sequence was used in an example illustrating an invention relating to a crystal of protein-ligand complex, which comprises an N-terminal truncated factor VIII and a ligand. The crystal diffracts x-rays to determine the atomic coordinates of the protein-ligand complex to a resolution of more than 5.0 Angstrom. The N-terminal truncated factor VIII retains the C2 domain of, and lacks at least 2000 amino acids from the flexible N-terminus of, the full-length factor VIII. The crystal is useful in drug screening assays. The method comprises selecting a potential ligand by performing structure-based drug design with a three-dimensional structure determined for the crystal preferably in conjunction with computer modelling. The potential ligand is contacted with the ligand binding domain of factor VIII and the
     binding is detected. A potential ligand is selected as a potential drug on the basis of its binding to the ligand binding domain of factor VIII with a similar affinity to a standard ligand, such as
                                                                                                                                                                                                                                                                                                                                                   Crystals of protein-ligand complex useful for developing new therapeutic drug agents, comprises carboxy terminal C2 domain of human blood coagulation factor VIII and a ligand -
                                                                                                                                                                                                                                                                                                                     Example; Page 60-64; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-211229/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stoddard BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-2000; 2000WO-US22226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; factor VIII; crystal; protein-ligand complex; C2 domain; drug screening; coagulation inhibitor; haemophilia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human factor VIII C2 domain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF60309 standard; cDNA; 9029
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glycerophosphorylserine,

phosphate

or sulphate.

The method is useful for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9029 BP; 2860 A; 1910 C; 1848 G; 2411 T; 0 other;
                                                                                                                                 AAV15359 standard; DNA;
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                                      Factor VIII; blood clotting;
                                                          Human Factor VIII DNA.
                                                                                   20-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                        488
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                        retrovirus; vector; human;
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                                     haemophilia
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Best Local Similarity
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03-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells, is resistant to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemophilia A patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (see AAW44373). The invention relates to preparations of replication defective recombinant retrovirus (RV) expressing a B domain-deleted human Factor VIII protein, such as the SQN deletion mutant (see AAW44372), where the recombinant RV is capable of infecting human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW44373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-086967/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9068 BP; 2885 A; 1908 C; 1867 G; 2408 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 28; Page 164-166; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain-deleted human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence includes a coding region for human Factor VIII AAW44373). The invention relates to preparations of replic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ı JR,
ı Vega
           cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga
                                                                                                                  aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac
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                                          cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                       cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta 731
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Barber JR, Boder M, Chang SM, Chon
D, Depolo NJ, Greengard J, Hsu DC,
Mittelstaedt DM, Prussak CE, Respes
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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96US-0645601
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96.2%;
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Pred. No. 4.3
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Search completed: January 8, 2002, 17:31:47 Job time: 12887 sec

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Result
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Listing first 45 summaries
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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4 US-09-324-867-1
1 US-08-212-133A-7
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2 US-08-670-707A-5
4 US-09-037-601-5
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US-09-243-539-1
US-08-366-8518-1
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Compugen Ltd
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Sequence 14, Appl
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Sequence 13, Appli
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ce: Synthetic	Artificial Sequen	; SEQ ; II ; O ; O US-09	
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	ALIGNMENTS		
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FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                             Sequence 14, Applica Patent No. 6221349 GENERAL INFORMATION:
                                                                                                          APPLICANT: Couto, Linda B. APPLICANT: COlosi, Peter C. TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS
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LENGTH:
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CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
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TITLE OF INVENTION: by Target Cells
FILE REFERENCE: Avigent,04082
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NUMBER OF SEQ ID NOS: 15
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                               tecaceatgeaaatagageteteeacetgettettetgtgeettttgegattetgettt
                                             tccaccatgcaaatagagctctccàcctgcttctttctgtgcctttttgcgattctgcttt 469
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86.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09364862 Patent No. 6221349
                                                                                                                                                                                                                                    SEQ ID NO 13
                                       Query Match
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/364,862

CURRENT FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER FILING DATE: 1999-03-24

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS FILE REFERENCE: AVIGEN-03743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Couto, Linda B. APPLICANT: Colosi, Peter C.
                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                  FEATURE:
                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                LENGTH: 11933
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                   73.6%;
86.1%;
    0;
Score 736.2; DB 4;
Pred. No. 4.4e-222;
0; Mismatches 118;
                                          Length 11933;
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    23; Gaps
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tttggtcgcccggcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatc 132 cayctycyctcyctcyctcactyayyccycccyyycaaagcccyyyycytcygycyacc

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RESULT 5
US-08-882-083-1
                                                                                  Sequence 1, Application US/08882083 Patent No. 5869292
                                                                   GENERAL INFORMATION:
   APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: .17
CORRESPONDENCE ADDRESS:
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US-08-882-083-1
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REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFX: 904136
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 600; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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STREET: 3000 K St.
CITY: Washington
STATE: D.C.
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                               aggtcctaccatccaggctgaggtttatgatacagtggtcattacacttacagacatggc
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                                                                TTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGC
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Pred. No. 8e-177;
0; Mismatches 13;
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US-08-558-107-1
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APPLICATION NUMBER: US/08/558,107
FILING DATE: 13-NOV-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
NUMBER OF SEQUENCES: N 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
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                                                                                                                                                                                                                                                                                                                         FEATURE:
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REFERENCE/DOCKET NUMBER: 30
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                                                                67 GTGCCTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACT
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Pred. No. 8e-177;
0; Mismatches 13;
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Patent No. 6130203
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                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY NUMBER OF SEQUENCES: 17
         SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
                                                                    REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                             TELEFAX: 1-1904136
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                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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US-09-243-539-1
                                                                                           GENERAL INFORMATION:
APPLICANT: Bodner,
APPLICANT: De POlo,
APPLICANT: Hsu, Day
APPLICANT: Chang, S
                                                                                                                                                           Sequence 1, Application US/08366851A Patent No. 5681746
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Best Local
                                           CORRESPONDENCE ADDRESS: ADDRESSEE: Viagene,
                                                                 APPLICANT: Chang, Steven
TITLE OF INVENTION: Retroviral Delivery
NUMBER OF SEQUENCES: 3
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    STREET:
CITY: S
STATE:
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TOPOLOGY: lin
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California 💌 🐧
                        E: Viagene, Inc.
11055 Roselle Street
                                                                                                    Bodner, Mordechai
De Polo, Nicolas J.
Hsu, David Chi-Tang
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35..5017
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Pred. No. 8e-177;
0; Mismatches 13;
                                                                            of Full Length Factor
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US-08-366-851A-1
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Best Local Similarity 96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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ATTORNEY/AGENT INFORMATION:
                     912
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TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 930049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/366,851A
                                                                                                            CACTTAACAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTTGGTGTATCCTACTGGA
tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                   aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa
                                                                                                                                                                                                                                                                                                                         aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac
                                                 AAGTCTTCCCTGGTAGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
                                                                                                                                                                                                                                                          cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
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110..7165
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Pred. No. 3.6e-176;
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                                                                            Query Match
Best Local Similarity
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                                                               Matches
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lollar, John S. APPLICANT: Runge, Marschall S. TITLE OF INVENTION: Hybrid Hun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                     372 actgacatccacttttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
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LOCATION: 5001 . 7053,
OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2
OTHER INFORMATION: domain",
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/
FILING DATE: 07 APRIL 1992
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                                                                                                                                                       OTHER INFORMATION: /note= "OTHER INFORMATION: domain"
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                                                                                                                                                                                    NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 2277
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                                                                                                                                                                         /note= "Equivalent to the Al-A2
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                                                                              Score 589; DB 1; Pred. No. 1.1e-175;
                                                                 Mismatches
                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                       CITY: Atlanta
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Sequence 3, Application US/08251937A Patent No. 5583209
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                                           APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
                         FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 31-MAY-1994
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
REFERENCE/DOCKET NUMBER:
                REGISTRATION NUMBER:
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TELECOMMUNICATION INFORMATION:

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NFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 TGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5001 . 7053
OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9009 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                tggcctctgacccactgtgctttacctactcatatctttctcatgtggacctggtaaaag 971
                                                                                      aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa 911
                                                                                                                                         CACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGA 526
                                                                                                                                                                                                                                    cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga
TGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAG
                                                                     AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA 646
                                                                                                                                                                                                                                                                                     CCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTA 466
                                                                                                                                                                                                                                                                                                                                                              AAAAGACTCTGTTTGTAGAATTÇACGGTTCACCTTTTCAACATCGCTAAGCCAAGGCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTAACCTTTTGCTTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapien
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96.0%;
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Pred. No. 1.1e-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Matches 604; Conservative

Local Similarity

58.9**%**; 96.0**%**;

Score 589; DB 1; Pred. No. 1.1e-175;

Length 9009;

Indels

0;

Gaps

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0;

Mismatches

Best

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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-212-133A-1
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                     FEATURE:
                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                        TISSUE TYPE: Liver FEATURE:
                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: March 1:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                              NAME/KEY:
LOCATION:
                                                                                                                NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
                                                                                                    OTHER INFORMATION:
                                                                                                                                                                    OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                  NAME/KEY: misc_feature (Domain Structure) LOCATION: 5125 7053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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100 Peachtree Street
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                /note=
VIII."
                                                                                                                                                                  /note= "Equivalent to the A3-C1-C2 domain"
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                                                                                                "Equivalent to the
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                            "cDNA encoding human factor
                                                                                                A1-A2 domain."
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                     APPLICANT: Emory University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
           ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                       STATE: G
COUNTRY:
                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   FILING DATE: 07
CLASSIFICATION:
                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                 CITY: Atlanta
                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                            ADDRESSEE:
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccacctgcttctttctgtgccttttgcgattctgctttagtgccaccagaagatactacc 491
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Y: US
                                                                                                                                                                                                                                 1100 Peachtree Street,
                                                                                                          PatentIn Release #1.0,
                                                                                                                                                                                                                                              Kilpatrick & Cody
                                                           UMBER: US/08/474,503
07-JUN-1995
 EMU106CIP(3)
                                                                                                                                                                                                                                  Suite
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OTHER INFORMATION: OTHER INFORMATION: VOTHER INFORMATION: VUS-08-474-503-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
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LOCATION:
                                                                             527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature (Domain Structure) LOCATION: 5125 . . . 7053 CTHER INFORMATION: /note= "Equivalent to OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                         AAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACATCGCTAAGCCAAGGCCAC
                                                                                                                                                                                                                                                                                        ACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGTGTACA
tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                                                                                                                                   CCTGGATGGGTCTGCTACCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604;
                           AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
                                                                             Conservative
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1 . . . 2277
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96.0%;
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domain"
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VIII."
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Pred. No. 1.1e-175;
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: 303/499-0000 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                   MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 01 FILING DATE: 11-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/212,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASTFICATION: 435
PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: WO PCT/US94/13200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LOLLar, John S.

TITLE OF INVENTION: Hybrid Human/Animal Factor VIII

NUMBER OF SEQUENCES: 40

ANDRESS:
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                    FEATURE:
                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                          OTHER INFORMATION: /product= "Domain Structure"
OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2 domain"
                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 5125..7053
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    LOCATION:
                                                                                                                                                                                                        TISSUE TYPE:
                   NAME/KEY:
                                                                             LOCATION:
                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Greenlee, Lorance L
REGISTRATION NUMBER: 27,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO POSTLING DATE: 15-NOV-1994
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CITY: Boulder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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   misc_feature
1..2277
                                                                                             misc_feature
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SYSTEM: PC-DOS/MS-DOS
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                                               "Equivalent to the A1-A2 domain"
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                                                                                                                                                                                                                              Sequence 1, Application US/09037601 Patent No. 6180371
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Best Local Similarity
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                                                                                                                                                                                                                 GENERAL INFORMATION:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                APPLICANT: Lollar, John S. TITLE OF INVENTION: Hybrid
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                912
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                                                            ZIP: 80303
                                                                                       CITY: Boulder
STATE: Colorado
                                                                                                                       STREET:
OPERATING SYSTEM:
                                                                       COUNTRY:
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                                                                            USA
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compatible
PC-DOS/MS-DOS
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ADDRESSEE: Greenlee, Winner and Sullivan, P.C STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
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                                                                    Hybrid Human/Animal Factor VIII : 40
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/note= "cDNA encoding human factorVIII"
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Pred. No. 1.1e-175;
0; Mismatches 25;
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526 851

791

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OTHER INFORMATION: /product= "Domain";
OTHER INFORMATION: /note= "cDNA encod"
US-09-037-601-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Matches
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INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: WO PRIOR DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/037,601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
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                      612
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US (FILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                     CCACCTGCTTCTTTCTGTGCCGTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACC 226
aaaagactctgtttgtagaattcacggatcaccttttbaacatcgctaagccaaggccac
                                                                           acgcaagatttccttcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca 611
                                                                                                                                                 tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
                                                                                                                            TGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGG
                                                                                                                                                                                                                                                                                                                                                      604;
                                                        ACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGTGTACA
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                                                                                                                                                                                                                                                                                                                                                                     58:98;
96.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "cDNA encoding human factorVIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Domain Structure"
/note= "Equivalent to the A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Domain Structure"
/note= "Equivalent to the A3
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                                                                                                                                                                                                                                                                                                                                                                    Score 589; DB 4;
Pred. No. 1.1e-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Equivalent to the A1-A2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length 9009;
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PCT-US93-03275-3
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                                                                                                                                                                                                     TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 30309 TOTAL COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
TOTAL SYSTEM: PC-DOS/MS-DOS
TOTAL SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lollar, John S. APPLICANT: Runge, Marschall S. TITLE OF INVENTION: Hybrid Hun
                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                      HYPOTHETICAL: 1 ANTI-SENSE: NO
                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: EM
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100
CITY: Atlanta
                                                                                                                            STRANDEDNESS:
                                                                                                                                             TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
     ORGANISM:
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                                                                                                                                                              9009 base pairs
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                                                                                                                                                                                                                      404-815-6555
 Homo sapien
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                                                                                                             linear
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: NAME/KEY: misc_feature
: LOCATION: 1.2277
: OTHER INFORMATION: /note= "Domain Structure:
: OTHER INFORMATION: Equivalent to the Al-A2 domain"
PCT-US93-03275-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE: Liver
FEATURE:

NAME/KEY: misc_feature
LOCATION: 5001..7053
OTHER INFORMATION: /note= "Domain Structure:
OTHER INFORMATION: Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
407
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                                                                                                                              672 cctggatgggtctgctaggttctaccatccaggctgaggtttatgatacagtggtcatta 731
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                                                              912
                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
                                        tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                                 aagtetteeetggtggäageeataeatatgtetggeaggteetgaaagagaatggteeaa 911
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Search completed: January  $\stackrel{4}{\cdot}$  8, 2002, 17:23:52 Job time: 12483 sec

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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 11351937 seqs, 5372889281 residues
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Gapop 10.0 , Gapext 1.0
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AA817854
AI526753
BG923886
BG9771142
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AI225600
BF150467
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2366.192 Million cell updates/sec
                                     BG923886 602824585
BG977142 602846744
AK014835 Mus muscus
AI225600 uj06c05.y
BF150467 uy86b07.y
BG862595 602795978
                                                                                                                                                                  Description
             AA865338
BE912296
                                                                                                                 AA817854 UI-R-AO-a
AI526753 uj42e03.y
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77.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7	MH175422	BE604025	//00C14B	221128986	8G976890	AI265337	BG568672	BE286923	BF122699	BF158434	BE283339	BF144018	BF383789	BG975622	BE285283	AI195667	BE308999	BG914512	BI428548	BF532535	AA873581	BF144665	BE917370	BE371524	в1107719	BF138391	BF136574	BG172588	BE916015	BE914540	AA461838	320
f. CTICLE	f 135h1	269696	CO20052	0118219	179548709	uk01h06	99/85209	60109269	60176122	f132g05.	6011022	60179127	60204470	60284532	60109827	u152c06.	60109709	60281325	tr85e10.	60207458	oh68a12.s	601791527	601666274	601223232	602892694	601782542	601779622	602337001	601666314	601665638	vf95d04.r	AV653260

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## ALIGNMENTS

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT BG477974 COMMENT VERSION ACCESSION DEFINITION FEATURES Locus TITLE JOURNAL source found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1408 row: c column: 17
High quality sequence stop: 626.
Location/Qualifiers Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/CTD/DTP 1 (bases 1 to 954)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. mRNA sequence. BG477974 BG477974 954 bp mRNA EST 21-MAR-2001 602522966F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4641352 5', Unpublished (1999) BG477974.1 GI:13410253 cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="IMAGE:4641352" /clone\_lib="NIH\_MGC\_20" /tissue\_type="melanotic melanoma"
/lab\_host="DH10B (phage-resistant)"

AL556703

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SOURCE
ORGANISM
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AA817854/c
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ORIGIN
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MEDLINE
                                                             JOURNAL
                                                                                                                                                                                                                                           AUTHORS
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Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                               discovery
                                                                                                                                                                 Normalization and subtraction: two approaches
                                                                                                                                                                                                                                     Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Ròdentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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89.1%;
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Pred. No. 1.5e-83;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds, mRNA sequence
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                                                                                                                                                                                                                      TCCTGGCGAGGGAGACAGCAATTGTGTGACCAGGATTTACCACTCTCATGTGGATGCTCC
                                                                                                                                                                                                                                                                                                                     TGACAAACTGTTTCCTGGACAGCAGTATTTGTACGTGCTGCGTGCC - - - AATGAGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                 CACCAAGGCGAACGAGGGGGCCATCTACCCTGACAACACCACTGATTTTCAAAGAGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTCACGTAAAGAACTTTGCCTCTAGGCCCTACACTTTTCATGCTCATGGGGTAACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult Ovary library.cDNA Library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics This clone is also available through the I.M.A.G.E.
Consortium at LLNL (info@image.llnl.gov). IMAGE ID-1767329
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451 Eckstein Medical Research Building
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Mar 9, 1998 this sequence version replaced gi:2946779 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_I: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung, brain
, liver, kidney, heart, spleen, ovary, and muscle. The tag
is a string of 3-5 nucleotides present between the Not I
site and the oligo-dT track which allows identification of
the library of origin of a clone within the mixture."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-A0-ae-g-10-0-UI"
/clone_lib="UI-R-A0"
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55.1%;
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Pred. No. 6.5e-18;
0; Mismatches 172;
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DEFINITION
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                                                                                    728 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctac 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. and Wilson,R. The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MarratM/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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AI526753
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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1 to 625)
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/sex="female"
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288 CCAGCCTGGCTAGGGTTTTTAGGCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 347
                     668 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 727
                                                                                         228 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                      /note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

a 131 c 148 g 177 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma'
/dev_stage="5 months"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E., Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10972 row: g column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 42 High quality sequence stop: 772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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    Conservative
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Library constructed by Life Technologies. In
providing Samples: Jeffrey Green, M.D., NIH"
a 161 c 176 g 210 t
                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Mam6"
/sex="female, Virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:4977442"
                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                   note="Organ; mammary; Vector: pcmV-SPORT6; Site_1: Sall;
                  9.98;
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  Score 98.6; DB 11;
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                                                                                    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer genome research. 10 (11), 1757-1771 (2000)
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AK014835.1
    The
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
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AL Nature 409, 685-690 (2001)
CE 5 (bases 1 to 3739)
RS Adachi J., Aizawa K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
                                           535 GTTCACTTAAAGAACCTTGCCTETAGGATCTACACTTTTCATGCACATGGGGTAACGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/db_xref="MGD:MGI:88476"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="testis"
/clone_lib="RIKEN_full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="4921507J22"
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                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%;
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98.6; DB 12; Pred. No. 1.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases 1 to 1006)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 463.
Location/Qualifiers
                                              Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTCGAGCTCGAGCACA."
                                                                                                                              ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pMELBS-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI show be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                             /note "Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDN was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:1891112"
                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL"
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Length 1006;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 286
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                                                                                                                                                                         Seq F
                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
BF150467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF150467 669 bp mrNA EST 29-DEC-2000 uy86b07.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666421 5's similar to SW:CERU_MOUSE Q61147 CERULOPLASMIN PRECURSOR;; mRNA
                                                                                                                                                                                                                    MGI:1427189
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
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1 (bases 1 to 669)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                            primer: -40RP from Gibco
                                                                                                                                                   quality sequence stop: 428.
Location/Qualifiers
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/clone="IMAGE:3666421"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
                                                                     /strain=(C57/B6"
/db_xref="taxon:10090"
                                                                                                            /organism="Mus musculus"
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54.7%;
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Pred. No. 1.3e-17;
0; Mismatches 175;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10828 row: k column: 19
                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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602795978F1 NIH_CGAP_Mam4 Mus
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                                                                                                                                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                         AA865338.1
Tissue Procurement: Christopher Moskaluk, M.D.,
                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                            Unpublished (1997) -
                                                                                       Tumor Gene Index
                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B"
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 360.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                 BE912296 878 bp mRNA EST 29-SEP-2000 601666013F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3966051 5',
                                                                            BE912296.1 GI:10409387
                                                                                                                BE912296
                                                                                                                                                 mRNA sequence.
house mouse
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/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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Pred. No. 5.2e-17;
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LOCUS AL556703 918 bp mRNA EST 16-FEB-200: DEFINITION AL556703 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK005Y102
                                                                 AL556703
                                                                                       RESULT 12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 attacacttaagaacatggcttccccatcctgtcagtcttcatgctgttggtgtatcctac 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                       GACAAAGTGCTTCCCGGACAACAGTATGTGTATGTGCTGCATGCC---AATGAGCCAAGT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 300
                                                                                                                                                                                                                                                CCTGGAGAGGGAGACAGCAATTGTGTGACCAGGATTTACCACTCCCATGTTGATGCTCCA 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999).
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 596.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
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a 188 c 195 g 227 t
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                            966 taaaagacttgaattcaggcctcattggagcccta 1000
                                                                                                              559 CAAAAGATATTGCCTCAGGACTCATCGGACCTTTA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 TATATAAGAAGGCCCTTTATCTTCAGTACACAGATGAAACCTTTAGGACAACTATAGAAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AACCGGTCTGGGTTTTTTAGGCCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 ggccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 tgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaa 665
                                                  13
                                                                                                                                                                                                                                                                                                    ATGACAAAGTATATCCAGGAGAGCAGTATACATACATGCTTGCCTTGCCACTGAAGAACAAA 498
                                                                                                                                                                                                                                                  gtccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctgg 965
                                                                                                                                                                                                                                                                                                                                               atgataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatg 905
                                                                                                                                                                                                                                                                                                                                                                                                 ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                  tcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcct 785
                                                                                                                                                                                                          GTCCTGGGGAAGGAGATGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208;
  AV653260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP 191 91006 EVRY cedex - rrance
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prime, market AL556703
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1 (bases 1 to 918)
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/clone_lib="LTI_NFLOO6_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6: Site_1: Not1; lst strand cDNA
/note="Vector: pCMVSPORT 6: Site_1: Not1; lst strand cDNA
was primed with a Not1:oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fillparth.iovitocom.com/
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169 c 192 g 253 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; 1 (bases 1 to 634)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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197 GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econe RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonaldo.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
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0; Mismatches 172;
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AUTHORS
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Matches 212; Conserv
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608 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 667
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 576)

NIH-MGC http://mgc.ngi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
plate: LLAM9137 row: l column:
High quality sequence stop: 576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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119 c 127 g 151 t 1 others
                                                                                                                                                                                                                                                                                                                                                                 /clone_ib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host, "DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                       GGAGAGG----GAGACAGCAATGTGTGACCAGGATTTACCACTCCCATGTTGATGCTCCA
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Search completed: January 8, 2002, 15:13:44 Job time: 4820 sec

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Maximum DB seq length: 200000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

ORIGIN	BASE COUNT		source	FEATURES	JOURNAL		TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR138378	RESULT 1
	1375 a 1151 c 1155 g 1318 t	/organism="unknown"		Location/Qualitiers	Patent: US 6200560-A 14 13-MAR-2001;	target cells	Adeno-associated virus vectors for expression of factor viii by	Couto, L.B., Colosi, P.C. and Qian, X.	1 (bases 1 to 4999)	Unclassified.	Unknown.	Unknown.		AR138378.1 GI:14480723	AR138378	Sequence 14 from patent US 6200560.	AR138378 4999 bp DNA PAT TO JON ZOOT		

961 cctcagtgagcgagcgagcgcgcagctgcctgcaggacat 1000 	Qу
901 gctcgctcactgaggcdgggcgaccaaaggtcgcccgacgcccgggctttgccc 	Дb
41 tttgtgtgcggccgca 	Дy
781 cototactgactcgagcotaataaaggaaatttattttcattgcaatagtgtgt 	Дb
721 ccagagittgggtgcaccagattgccctgaggatggaggttctgggctgcgaggca 	Ωу
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41 tetgettaceage	gy Qy
81 gcaagtggacttccagaaga	Db Qy
21 tcacctccaa               1	45 dd
361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctc	В 64 63
001 tttaaatagttgcagca 	, pp o
40	D Qy
181 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgataca 	D Qy
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61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgat	d da
1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggt	QУ
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                                                                        4000 GATCAAGGTGGATCTGTTGGCACCAATGATTATTCACGGCATCAAGACCCCAGGGTGCCCG 4059
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                       GTGGACTCTCTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT 4659
                                       9tggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
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Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated vectors for expression of factor VIII by target cells
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Sequence 14 from patent US 6221349.
AR146888
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TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA
                                                  tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                  GGATTCATCTGGGATAAAACACAATATTTTAACCCTCCAATTATTGCTCGATACATCCG
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Sequence 13 from patent
AR138377
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Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated virus vectors for
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Sequence 13 from patent US
AR146887
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Couto,L.B., Colosi,P.C. and Qian,X.
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                  ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga
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Seed, B. and Haas, J.
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tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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                                                                                                    GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                                gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcaggggagtaaaatc 540
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                                                                 tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 600
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Voorberg, J.J.
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                                               TCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAATCCAAAAGAGTGGCT
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                                                                                             TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT 4650
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Voorberg, J. J.
Hybrid proteins with
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                                             tttaaatagttgcagcatgccattgggaátggagagtaaagcaatatcagatgcacagat
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Sequence 1 from patent US
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177105
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Yonemura, H., Tajima, Y., Sugawara, K. and Masuda, K.
Process for preparing human coagulation factor VIII protein
Patent: US 5693499-A 1 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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Sequence 1 from patent.US. 127063
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                                                                                                                                                                                                                                                             Unclassified.
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Query Match Matches 793; Best Local

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4967)
Saenko,E.L. and Strickland,D.K.
Methods of reducing factor viii clearance and compositions therefor Patent: WO 0071714-A 1 30-NOV-2000;
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171409
                                                                                                                         Bodner,M., De Polo,N.J., Chang,S., Hsu,D.Chi-Tang and Respess,J.
Retroviral delivery of full length factor VIII
Patent: US 5681746-A 1 28-OCT-1997;
Location/Qualifiers
1. 8967
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Wood, W.I., Capon, D.J., Simonsen, C.C., Eaton, D.L., Gitschier, Keyt, B., Seeburg, P.H., Smith, D.H., Hollingshead, P., Wion, K.L. Delwart, E., Tuddenham, E.G.D., Vehar, G.A. and Lawn, R.M. Expression of active human factor VIII from recombinant DNA Nature 312 (5992), 330-337 (1984) 85061548

Data kindly reviewed (20-MAR-1986) by W. Wood.
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Human mRNA for X01179
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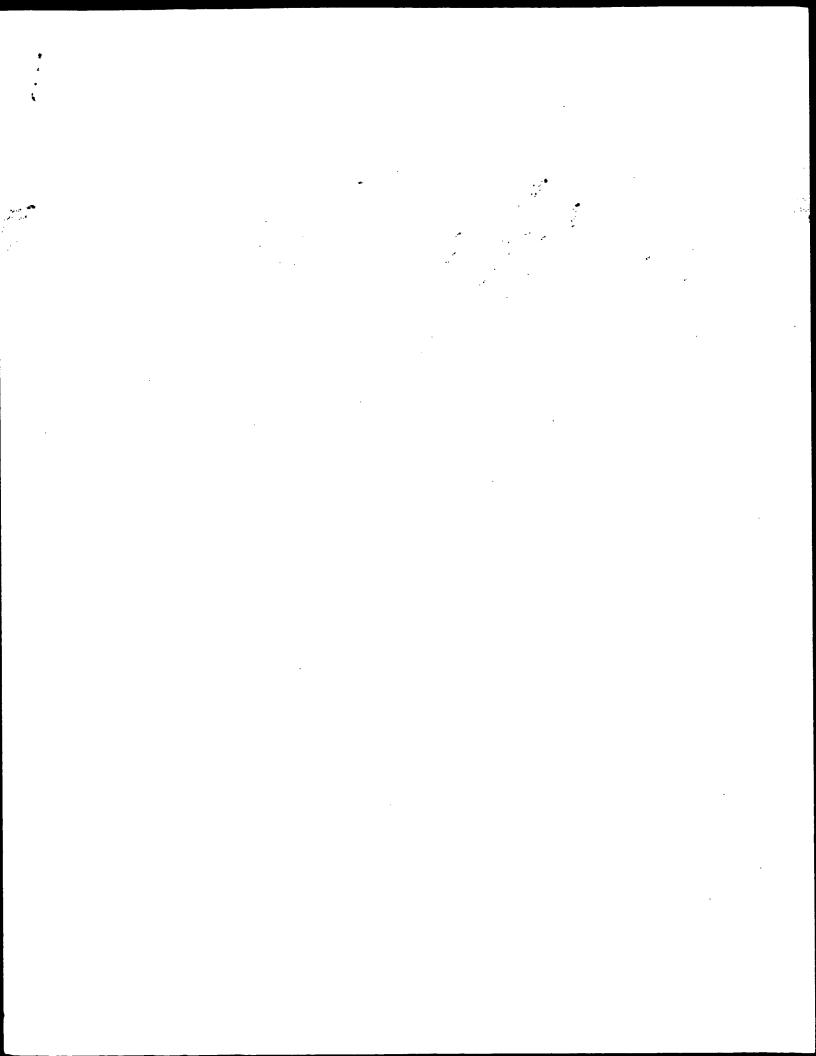
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DSFTPYVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY"
167. .7162
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SYEDISAYLLSKNNAIEPRSFSONSRHRSTRQKQFNATTIPENDIEKTDPMFAHRTPM
PKIQNVSSSDLLMLLRQSPTPHGLSLSDLQEAKYETFSDDPSPGAIDSNNSLSEMTHF
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/db_xref="taxon:9606
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TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
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RLPKGVKHLKDFPILIGEIFKY KWTVTVEDGPTKSDPACLTRYY SSFVNNERDLASGL
IGPLLICYKESVDQRRQIMSDKRNVILFSVFDENRSWYLTENIQRFLLNPAGVQLED
PEPQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMV
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IGMGTTPEVHSIFLECHTELVRNHRQASLDISPITELTAQTLLKUDLGQFLLFCHISSH
QHOGMEAYVKVDSCPEEPQLAKKNNEEAAEDVDDLTDSEEMDVNRFDDNSSPSTQITS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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Lollar, J.S. and Runge, M.S.
Hybrid human/animal factor VIII
Patent: US 5744446-A 1 28-APR-1998;
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                                                 gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc
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Search completed: January 8, 2002, 17:27:05 Job time: 12716 sec



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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

AAD00122

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AAD00122 standard; DNA; 4999 BP.
                                                                                         20-OCT-1998;
24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                      Recombinant Adeno Associated Vector; rAAV; pVm4.1cF8deltaB; promoter; human Factor VIII; hFVIII; EF1alpha; human elongation factor-lalpha; human growth hormone; hGH; ITR; inverted terminal repeat; haemophilia;
                                                                                                                                                                                                                                                                                    Recombinant adeno associated vector construct, pVm4.1cF8deltaB
                                                                                                                                                                                                                                                                                                           31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                  AAD00122;
                                                                                                                                                                                                                             gene therapy; ds.
                                                                                                                                                                                   WO200023116-A1.
New recombinant adenovirus-associated vector, useful for gene therapy
                                                                  (AVIG-) AVIGEN INC.
                                                                                                                                     19-OCT-1999;
                                                                                                                                                                                                       Adeno associated virus.
                        WPI; 2000-339536/29.
                                             Couto LB, Colosi PC;
                                                                                          98US-0104994.
99US-0125974.
99US-0364862.
                                                                                                                                       99WO-US24495.
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to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
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Example 9; Fig 6; 92pp; English

The present DNA sequence is a recombinant adenovirus-associated vector, C (rAAV) construct pVmA.lcP8deltaB. This expression vector comprises the promoter, first intron (-573 to +985) of human elongation factor-lalpha C (EFlalpha) gene, human Factor VIII coding sequence (hFVIII) and a C polyadenylation signal from human growth hormone (hGH). This sequence is first 57 bp encoding the 19 amino acid signal peptide, Al and A2 domains C and 5 amino acids from the N-terminus of the B domain. The light chain c segment comprises the heavy and light chain sequences into the same plasmid seperated by 42 nucleotides coding for 14 residues C of the B domain, that is deleted. This plasmid is operably linked to C control sequences, that directs the transcription and translation of the therapy to treat haemophilia. This method allows prolonged expression of therapy, because of their broad host range, safety profile and duration xx xx

Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other:

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nes 1000; Conservative
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The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is
                                                                                                              Claim 19; Fig 6; 90pp; English.
                                                                                                                                                  Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood
                                                                                                                                             coagulation factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Adeno associated virus.
Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                         WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                  (AVIG-) AVIGEN INC.
                                                                                                                                                                                                                                                                                            22-DEC-1999; 99US-0470618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             separated by 14 amino acids of the B domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4060 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 4119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4000 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4120 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 4179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                                                                                                                   4540 totgettaccagcatgtatgtgaaggagtteetcateteeageagteaagatggeeatea 4599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
                                                                                                                                                                                                                                                                              4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gatcaaggtggatotgttggcaccaatgåttattcacggcatcaagacccagggtgcccg
                                                                                                                                                                                              4660 cacacetgtggtgaactetetagaeceaecgttaetgaetegetaecettegaatteaece 4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
                                                                                                                 4720 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 4779
                                       4780 cctctactgactcgagcctaataaaggaaatttattttcattgcaatagtgtgttgttt 4839
                                                                                                                                                                                                               661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
                                                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                                                                                                        541 tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 600
                                                                                                                                    721 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 780
                                                          781 cctctactgactcgagcctaataaaggaaatttattttcattgcaatagtgtgttggttt 840
841 tttgtgtgcggccgcaggaacccctagtgatggagttggccactccctctctgcgcgctc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 4299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 4239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 4539
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                          gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 4659
                                                                                                                                                                                                                                                                                               gtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score 1000; DB 22;
pred. No. 5.6e-302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sequence 11933 BP; 3258 A; 2818 C; 2717 G;

3140 T; 0 other;

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                                hfvIII coding region comprises the heavy chain gene segment with the can and a main acid signal peptide, Al and A2 domains can are segment comprises the heavy and light chain gene segment comprises the C-terminal 85 amino acids of B domain. The light chain comprises the C-terminal 85 amino acids of B domain and the A3, compared to the same plasmid seperated by 42 nucleotides coding for 14 residues code the B domain, that is deleted. This plasmid is operably linked to control sequences, that directs the transcription and translation of the control sequences, that directs the transcription and translation of the control sequences, that directs the transcription and translation of the control sequences, that directs the transcription and translation of the control sequences, that directs the transcription and translation of the pay to treat haemophilia. This method allows prolonged expression of therapy to treat haemophilia. This method allows prolonged expression of therapy, because of their broad host range, safety profile and duration of expression in the infected hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4840 tttgtgtgcggccgcaggaacccctagtgatggagttggccactccctctctgcgcgctc 4899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD00121 standard; DNA; 11933 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1998;
24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hFVIII; HNF-3 albumin promoter; human elongation factor-lalpha; EFlalpha; human growth hormone; hGH; inverted terminal repeat; ITR; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant adeno associated vector construct, pAAV-F8-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD00121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200023116-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno associated virus
                                                                                                                                                                                                                                                                                                                                The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-laipha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII) factor-laipha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant adenovirus-associated vector, useful for gene therapy to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Couto LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVIG-) AVIGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-339536/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 5; 92pp; English.
                                                                                                                                                                                                                                                                                                   and polyadenylation signal from human growth hormone (hGH). This se is inserted between the AAV inverted terminal repeat (ITR) regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cctcagtgagcgagcgcgcgcagctgcctgcaggacat 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccggggctttgcccgggcgg 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nimeninimalandikaniminimananandikili
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0364862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0125974.
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4930 cctcagtgagcgagcgcgcgcgctgcctgcaggacat 4969
                                                                             4870 gctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggctttgcccgggcgg
                                                                                                                                                                4810 titgtgtgcggccgcaggaacccctagtgatggagttggccactccctctctgcgcgctc 4869
                                                                                                                                                                                                                                                  4755 cctctactgactcgagaataaaagatcagagctctagagat-----ctgtgtgttggttt 4809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                     4695
                                                                                                                                                                                                                                                                                                                                                                                                                          4635 cacacotytygytyaactototagacocacogttactgactogotacottogaattoacoc 4694
                                                                                                  901 gctcgctcactgaggccgggtgaccaaaggtcgcccgacgcccgggctttgcccgggcgg 960
                                                                                                                                                                                    841 tttgtgtgcggccgcaggaacccctagtgatggagttggccactccctctctgcgcgctc 900
                         961 cctcagtgagcgagcgagcgcagctgcctgcaggacat 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4575
                                                                                                                                                                                                                                                                                781 octotactgactcgagoctaataaaggaaatttattttcattgcaatagtgtgtttggttt 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4455 gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 4514
                                                                                                                                                                                                                                                                                                                                                              721 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                661 cacacctgtggtgaactctctagaacccaccgttactgactcgctaccttcgaattcaccc 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4395 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 totgottaccagcatgtafgftgaaggagttcctcatctccagcagtcaagatggccatca 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4275 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 4334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4215 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 4274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3975 gatcaaggiggatcigitiggcaccaatgattattcacggcatcaagacccagggigcccg 4034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                                                                                       ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga 4754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 4634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9t9gactctctttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 4574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 4394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 4154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.4%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 954.4; DB 21; Length 11933; Pred. No. 1.7e-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 16; Indels
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В Ş В δÃ 밁 Qγ В Qy 밁 δÃ В δÃ В δÃ Ъ Ş В Ş В 5 В Ş В δõ В Qγ 밁 ρy В Q Дb Ş ₽

QΥ DЬ δÃ В

4035 tcagaagttotocagoototacatototoagtttatcatoatgtatagtottgatgggaa 4094

61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120

121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180

3975 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 4034

1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60

Matches Query Match

979;

Conservative

Mismatches

16;

Indels

5; Gaps

1;

Local Similarity

95.4%; Score 954.4; DB 22; Length 11933; 97.9%; Pred. No. 1.7e-287;

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AAD08612
Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                  backbone. It comprises HF-3 mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EFlalpha) and immunoglobulin G (IGG) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the light and heavy chains of human factor VIII.
                                                                                                                                second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is particular humans. The rAAV vector provides high level and long term expression of biologically active clotting factor VIII in vivo.

The present sequence is pAAV-FB-1 vector without the plasmid
                                                                                                                                                                                                                                    administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a
                                                                                                                                                                                                                                                                         The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises
                                                                                                                                                                                                                                                                                                                                    Claim 18; Fig 5; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                               Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood coagulation factor {\tt VIII}
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Couto LB, Colosi PC,
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Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AVIG-) AVIGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Adeno associated virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blood clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
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                                                              Plasmid DLZ6 encoding human B-domain deleted factor VIII.
                    coagulation disorder; ss.
                                 Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
                                                                                                   29-JUN-2001
                                                                                                                                                                                                                                                               961 cctcagtgagcgagcgagcgcagctgcctgcaggacat 1000
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                                                                                                                                                                                                                                                                  vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one enhancer and at least one promoter. The method results in the production of high titer rAAV vector stocks carrying the B-domain deleted factor VIII transgenes and expression cassettes, which generate adequate titers of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded B-domain deleted factor VIII, which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a recombinant adeno-associated virus (rAAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 64; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-273781/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression control element -
                                                                                                                                                                                                                                          Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
4046 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 4105
                                                                                                                                                                       Local Similarity
les 933; Conserv
                                                                      61 toagaagttotocoagoototacatototoagtttatoatoatgtatagtottgatgggaa 120
                                                                                                                            1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
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                                                        tcagaagttotocagoototacatototoagtttatoatoatgtatagtottgatgggaa 4165
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                                                                                                                                                                         Conservative
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/note= "human B-domain deleted factor VIII"
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/note= "hepatitis B virus EnhI enhancer"
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/note= "TK polyA sequence"
                                                                                                                                                                                        87.1%;
92.7%;

 Mismatches

                                                                                                                                                                                        Score 870.8;
Pred. No. 1.8
                                                                                                                                                                                              1.8e-261;
                                                                                                                                                                                                            DB 22;
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                                                                                                                                                                                                            Length 7944;
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Homo sapiens.
                                                   Human Factor VIII:C;
                                                                           DNA encoding 740 Arg-1649 Glu human Factor VIII:C.
                                                                                                                                                               AAN90654;
                                    haemophilia A.
                                                                                                                           26-JUN-1990
                                                                                                                                                                                           AAN90654 standard; DNA; 4275 BP.
                                                                                                                                                                                                                                                                                            5006
                                                                                                                                                                                                                                                                                                                                                                                                               4886 gcacgggtgttgggtcgtttgttcggatccagatctaggaacccctagtgatggagttgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca
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                                                                                                                     (first entry)
                                     Ad.RE.neo; 740 Arg-1649 Glu Factor VIII:C;
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                              3846 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 3905
                                                                                           3786 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat
                                                                                                                                                         3726 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                                                                                                                                                        3606 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 3665
421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                                                                                                   3546 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                3486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    When translated, Arg-740 of the carboxyl terminus of the H chain is directly bonded by a peptide bond to Glu-1649 of the amino terminus of L chain. It is used to transform animal cells so that they produce The Aprentice Aprentice Appression vector is plasmid Ad.RE.neo. The expression vector has at least one promoter upstream of AAN90654. The transformants can constantly and continuously produce human Factor VIII:C in high yield on a commercial scale. The human Factor VIII:C so intact Factor VIII:C molecules in the human blood plasma. It is useful
                                               361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                                                         241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4275 BP; 1245 A; 941 C; 945 G; 1144 T; 0 other:
                                                                                                                                                                                                                                                                                                       121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating haemophilia A patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of recombinant human Factor-VIII-C - using animal cells transformed with a vector contg. the gene for % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 1(1) - 1(13); ; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Factor VIII:C and a promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAP91165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA ) CHEMO-SERO-THERAP (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                               gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 3545
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1..4275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.0%; Score 790; DB 10; 1 100.0%; Pred. No. 2.4e-236;
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                                                                                                                                                                                                                                      07-JUN-1995;
10-JUN-1993;
25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX88293 standard; DNA; 4629 BP
                                                                                                                                                                                                                                                                                                                                                                                                                              Human Factor VIII with B domain deleted cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX88293;
                                                                                                                                                                                                                                                                                                                                           US5935935-A.
                                                                                                                                                                                                                                                                                                                                                                                        Adenoviral vector; Factor VIII; Factor IX; clotting factor; treatment; haemostatic; haemophilia \hat{A}; haemophilia \hat{B}; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                 10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 cctctactga 790
                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                   This invention describes movel adenoviral vectors comprising at least one DNA sequence encoding a clotting factor (Factor IX or Factor VIII). The vectors of the invention have haemostatic activity. The vectors are useful for the treatment of hemophilia A or hemophilia B by gene therapy. This sequence represents human Factor VIII cDNA which has the B domain
                                                                                                                                                                                        Connelly S,
                                                                                                                                                                                                              (GENE-) GENETIC THERAPY INC
                                                                                                                                                                WPI; 1999-457617/38.
                                                                                                              Example 1; Column 53-58; 90pp; English.
                                                                                                                                   Adenoviral vectors useful for treating hemophilia
 Sequence 4629 BP; 1319 A; 1050 C; 1015 G;
                           deleted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cctctactga 4275
                                                                                                                                                                                           Kaleko M,
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93US-0074920.
94US-0218335.
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             1245 T; 0 other
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                                                                                                                             AAV23339 standard; DNA; 4670
                                       Human Factor-VIII gene lacking central B domain.
                                                                                                  AAV23339;
                                                                                                                                                                                                                                                                           721 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgagggcacagga 780
            Factor-VIII; blood clotting; human;
                                                                       17-AUG-1998
                                                                                                                                                                                                                                781 cctctactgactcgagcc 798
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                                                                                                                                                                                                                                                                                                                                      cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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Pred. No. 2.5e-236;
                      synthetic gene;
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                           codon usage;
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                                                                   4073 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4132
                                                                                                                              4013 tactgetteateetåetttaecaatatgtttgeeaeetggteteetteaaaagetegaet 4072
                                                                                                                                                                                           3953 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 4012
                                                                                                                                                                                                                                                        3893 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                421 tcacctccaagggaggagta&tgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                                                                     3833 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 3892
                                                                                                                                                                                                                                                                                                                                                                             3773 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttcttttggcaatgt 3832
                                                                                                                                                                                                            301 tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                                                                       241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel, claimed synthetic gene (see AAV2328B), non-preferred or less preferred codons of the native gene are replaced by codons expression in mammalian cells. The synthetic gene was assembled PCR templates. Synthetic genes of the invention (see also AAV232B9 91) are used for production of recombinant proteins in the natural genes. They can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3653 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 3712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4670 BP; 1325 A; 1072 C; 1036 G; 1237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This gene codes for a human Factor-VIII protein that lacks the central B domain (amino acids 760-1639) of the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 tcagaagttctccagcctctaca&ctctcagtttatcatcatgtatagtcttgatgggaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 12; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic eukaryotic gene(s) - in which non-preferred or less preferred codon(s) are replaced to provide high level expression mammalian cell(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gatcaaggtggatctgttggcaccaatgattattćacggcatcaagacccagggtgcccg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loca!
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                                                                                                                                                tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                                                                                                                                                                                                                     99attcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                                                                                                                                                                                                                                                                                                                                                          tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 3772
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0;
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This cDNA encodes the beta-domain deleted SQN deletion protein of human

Example 28; Pages 210-213; 272pp; English.

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                                                  administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable
                                                                              New replication defective recombinant retro-viruses - which can be
                                                                                                                                                                                                                                                         04-JUN-1997;
03-JUL-1996;
13-AUG-1996;
                                                                                                                          P-PSDB; AAW46246.
                                                                                                                                      WPI; 1998-086966/08.
                                                                                                                                                                                   De LA VEGA D,
                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                     Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Guacher's syndrome; high blood pressure; Alzheimer's disease, autoimmune;
                                                                                                                                                                                                                                                                                                                02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                    W09800541-A2
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                         Barber JR, Boder M, Chang SMW, Chong K;
A D, Depolonj, Greengard J, Hsu DC, Iban
Lee R, Mittelstaedt DM, Prussak CE, Res
                                                                                                                                                                                                                                                    96US-0696381
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                                                                                                                                                                         Ibanez CE;
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CC degradation by human complement and is capable of inducing long term CC degradation by human complement and is capable of inducing long term CC systemic expression of the therapeutic protein when administered CC intravenously to a human. The long term systemic expression results in a CC intravenously to a human. The long term systemic expression results in a CC of the human for a period of at least 30 days after the administration of CC therapeutic protein to treat, e.g. haemophilia A, haemophilia B, CC thrombosis, hypercoagulable disorders, liver diseases such as helassemia, phenylketonuria, Lesch Nyhan syndrome, CC disorders such as thalassemia, phenylketonuria, Lesch Nyhan syndrome, CC severe combined immunddefiatency (SCID), cystic fibrosis, Duchenne's severe combined immunddefiatency (SCID), cystic fibrosis, Duchenne's cCC miscular Dystrophy, inherited emphysema, familial hypercholesterolemia, CC diabetes, hypopituitarism, adenine deaminase deficiency, alphaicantification, high blood pressure, Allheimer's disease, autoimmune or CC inflammatory disease or graft versus host disease, autoimmune or Surviving inactivation in human serum thereby allowing efficient gene CC transfer over prolonged periods of time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV)
Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;
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Query Match Best Local

79.0%;

score 790; DB 19;
pred: No. 2.6e-236;

рв 19;

Length 4832;

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les 793; Conserv
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                                                                                                                                                   gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
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gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 4315
                                                                                  totgottaccagodegtatgtgaaggagttcotcatotccagcagtcaagatggccatca 600
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                                                                                                                                gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 4195
                gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
                                                                  totgottaccagcatgfatgtgaaggagttcctcatctccagcagtcaagatggccatca 4255
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03-JUL-1996;
13-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Factor VIII; blood clotting; haemophilia A; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Factor VIII SQN deletion mutant DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retrovirus; vector;
pactor VIII, the SQN deletion does not influence the in vivo pharmacokinetics, but the reduced size of the molecule appears to decrease proteolytic degradation. The invention relates to preparations of replication defective recombinant retrovirus (RV) expressing a B domain-deleted human Factor VIII protein, where the recombinant RV is capable of infecting human cells, is resistant to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemophilia A patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1997;
                                                                                                                                            deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-743 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 and A3 Factor VIII domains. When compared to plasmid-derived and A3 Factor VIII domains.
                                                                                                                                                                                                                                 Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW44372.
                                                                                                                                                                                                                                                                                                                                       WPI; 1998-086967/08.
                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                     This DNA sequence includes a coding region for the B domain
                                                                                                                                                                                                                                                           treatment of haemophilia
                                                                                                                                                                                                                                                                        domain-deleted human factor VIII or human factor IX for the
                                                                                                                                                                                                                                                                                        New replication defective recombinant retroviruses - which express B
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Vega
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NJ, Greengard J, Hsu DC, Ib
L DM, Prussak CE, Respess JG
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Best Local
                  10-AUG-1997
                                                                                                                                              4436 cctctactgagggtggcc 4453
                                                                                                                                                                                                 4376 ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga
                                                                         AAT69811 standard;
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                                                                                                                                                                 781 cctctactgactcgagcc 798
                                                                                                                                                                                                                                                                          661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 79.0%; Sc
Local Similarity 99.4%; Pr
                                                                                                                                                                                                                   ccagagttgggtgcaccagattgccctgaggatggaggttctggggtgcgggggcacagga 780
                                                                                                                                                                                                                                                              cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 4075
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(first entry)
                                                                           DNA;
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Pred. No. 2.6e-236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB.19; Length 4832;
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                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                         Matches 793; Conservative
                                                                                                                                                                                                                                                                                          Best Local Similarity
4411 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                                                                                                                                                                                                                                                                                         A DNA molecule (AAT69811) codes for Factor VIII-dB695-HCII (AAW18670), a hybrid protein in which amino acids 712-736 of Factor-dB695 (Factor VIII de1868-1562) B-domain are replaced by amino acids 51-80 from the acidic region (and potential thrombin-binding site) of human heparin cofactor II (HCII). It was obtd. by PCR amplification (see also AAT69812-13) of the HCII acidic region from total liver cDNA, fusion to sequences encoding Factor VIII aa706-711 and aa737-743, and incorporation of the construct into plasmid pCLB-dB695. The hybrid protein, which can be expressed using gene therapy techniques, has increased procoagulant activity owing to the HCII acidic region, and can be used to treat blood coagulation disorders such as haemophilia A.
                                                                                                                                               4291
                                                                                                                                                                                                                                                                                                                                                 Sequence 5035 BP; 1484 A; 1127 C; 1110 G; 1314 T; 0 other;
             181 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 52-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           donor anticoagulant or antithrombotic protein - useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybrid Factor VIII with modified activity, comprises region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW18670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_RNA
                                                                                                                                                61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Factor VIII-db695-HCII; heparin cofactor II; blood coagulation; blood clotting; procoagulant; anticoagulant; antithrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Factor VIII-dB695-HCII DNA.
                                                                                                                                                                                                                 1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg
                                                             gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 4410
                                                                              gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttcttttggcaatgt 180
                                                                                                                                 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= heparin cofactor II region (aa51-81)
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35..5020
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                                                                                                                                                                                                                                                                  79.0%; Score 790; DB 18; 99.4%; Pred. No. 2.6e-236; ^. Mismatches 5;
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                                                                    4651
4711 gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 4770
                                                                                                                                                                      361
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                                                                                                      421
                                                                                                                                  tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 360
                                                                                    tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                                     tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                     gcaagtggacttccagaagacaatgaaagtcaccaggagtaactactcagggagtaaaatc 540
                                                               tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4710
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Qγ В Š Ş DЬ Qy В Ş 밁 4771 totgottaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 4830 4891 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 4950 5011 cctctactgagggtggcc 5028 541 totgottaccagcatgtatgtgaaggagttoctcatotocagcagtcaagatggccatca 600 781 cctctactgactcgagcck.798 ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga 5010 | ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga 780 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720

RESULT 12 AAA49231 AAA49231 standard; DNA; 5094 BP.

26-SEP-2000 (first entry)

Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract; haemophilia; Factor VIII; human; transgene; adenosine deaminase deficiency; ss; sickle cell anaemia; thalassemia; diabetes; alpha-antitrypsin deficiency; Alzheimer's disease; brain disease; heart disease; immune system defect; DNA construct HSQ/eGFP for transforming endothelial cells. fracture; osteoporosis.

WO200032750-A1

08-JUN-2000 24-NOV-1999; 99WO-US28033.

(MINU ) UNIV MINNESOTA. (UYEM-) UNIV EMORY. (HEBB/) HEBBEL R P. 24-NOV-1998; 98US-0109687

> (LOLL/) LOLLAR J S (LINY/) LIN Y

Hebbel RP, Lin Y, Lollar JS;

endothelial growth factor collagen I coated surface in culture medium comprising vascular Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with

Claim 19; Fig 3; 53pp; English.

RX
CC endothelial cells (EC) obtained for expanding the population of CC in contact with a collagen I coated surface, buffy coat cells obtained CC in contact with a collagen I coated surface, buffy coat cells obtained CC in contact with a collagen I coated surface, buffy coat cells obtained CC in containing vascular endothelial growth factor (VEGF) and free of bovine CC containing vascular endothelial growth factor (VEGF) and free of bovine CC into the blood stream of a mammal, so that an effective amount of CC pactor VIII protein is secreted in the blood stream of the mammal. CC This sequence represents a huamn factor VIII gene into which an CC enhanced green fluorescent protein coding sequence has been inserted. CC protein (eGFP); the last panino acids of the SQ linker peptide; an enhanced green fluorescent CC clomain and the hfVIII C2 domain. Transgenic EC transduced in vitro CC are useful for improving prosthetic implants. EC is also useful for cCC diagnosing clotting disorders where indication or disease is associated with a reduction in the activity of an enzyme. EC is also useful in gene CC deaminase deficiency, sickle cell anemia, thalassemia, hemophilia, CC transition boas frantitres and to transformer such as a cc contains the activity of an enzyme. EC is also useful for deaminase deficiency, sickle cell anemia, thalassemia, hemophilia, cc contains the protein contains the activity of an enzyme. EC is also useful for a contains the protein contains the activity of an enzyme. EC is also useful for a contains the protein contains the activity of an enzyme. EC is also useful for a contains the protein contains th repairing bone fractures and to treat or prevent osteoporosis.

Sequence 5094 BP; 1435 A; 1207 C; 1169 G; 1283 T; 0 other;

Query Match

Local Similarity

100.0%;

79.0%; Score 790; DB 21; 100.0%; Pred. No. 2.7e-23

.7e-236;

0;

Gaps

Length 5094; Indels

QY 망 γ Дb δÃ 밁 QΥ 밁 밁 Вb Matches 4305 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 4364 4365 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 4545 4425 181121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttcttttggcaatgt 180 61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 4484 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 790; Conservative 0; Mismatches 0 4424 4664 4604 420

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RESULT 13
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                                Disclosure; Page 27-36; 61pp; English.
                                                                                 Nucleic acid encoding porcine factor VIII
                                                                                                                                         Kaufman RJ, Pittman D, Rehemtulla A,
                                                                        porcine and human-porcine chimeric factor VIII
                                                                                                                P-PSDB; AAR55352.
                                                                                                                                                                              (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                     13-NOV-1992;
                                                                                                                                                                                                         14-SEP-1993;
                                                                                                                                                                                                                                              01-OCT-1993;
                                                                                                                                                                                                                                                                       26-MAY-1994.
                                                                                                                                                                                                                                                                                                 W09411503-A
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           Factor VIII; haemostasis; haemophilia A; clotting cascade;
fibrinogen; fibrin; thrombin; proteolytic enzyme; co-factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ66615 standard; cDNA; 7056 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ66615;
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                                                                                                                           1994-183504/22.
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93US-0121202.
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                                                                                                                                                Wozney Jм;
                                                                                 · used to obtain
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Prepn. of human factor VIII cDNA has been set forth in detail, e.g.,

Patent No. 4,757,006 issued July 12, 1988 and in Toole et al.,

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Best Local
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721 ccagagttgggtgcaccagattgccctgaggattggaggttctggggctgcgaggcacagga 780
                                                                                          661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               include those where various domains of the human factor VIII have been replaced, in whole or in part, by analogous porcine factor VIII in whole or in part, of the human factor VIII and the porcine factor VIII in whole or in part, of the human factor VIII sequence have been porcine factor VIII. Specifically provided are chimeric factor VIII sequence factor VIII. Specifically provided are chimeric factor VIII sequences comprising the Al. A2, A3, B, C1 and C2 human domains as set forth in AAQ66615, where the Al and/or A2 domains, as well as other segments, such as the regions corresp. to the AA numbers 336-372, 336-740, 372-740, 700-740 and combinations of these regions have been replaced in whole or in part with porcine factor VIII sequences as set forth in AAQ66616 and AAR55353.
                                                                                                                                                                                                                                                                                                                                                                                                                                            421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                     totgottaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca
                                                                                                                                                      gtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt
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Pred. No. 3.2e-236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1996 (first entry)
                                                                                                                                                                                  (AAW00465), a trace plasma glycoprotein which acts as a cofactor in conjunction with Factor-TXA in the activation of Factor-TX. Retroviral vectors comprising the full-length cDNA can be efficiently packaged into infectious retroviral particles. These may be used to transduce cells either in vivo or ex vivo. Factor-VIII expressed from such transduced cells will be processed and transported in a fashion analagous to the expression product of a normal Factor-VIII gene. Retroviral particles harbouring such vectors will be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
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                                                                                                                                                                                                                                                                                                                                    Retroviral vector directing expression of full length factor VIII used in the gene therapy and treatment of haemophilia A
                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW00465.
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                                                                                                                                                 Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                                                                                                                                                                                                                    A full-length cDNA clone (AAT31031), codes for human Factor VIII
                                                                                                                                                                                                                                                                                                               Claim 3; Page 58-68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON VIAGENE INC
              61
                                               1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
                                                                                                                                                                        the gene therapy of haemophilia A.
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           tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
                                   gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 6435
Similarity
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                                                                                                                                                                                                                                                                                                                     AAC87526 standard; DNA; 8967 BP
                                                                                                                                                                     Factor VIII; human; A2 domain; C2 domain; LRP-mediated plasma clearance;
                                                                                                                                                                                                              Human factor VIII cDNA, SEQ ID NO:1.
                                                                                                                                                                                                                                                  13-MAR-2001 (first entry)
24-MAY-2000; 2000WO-US14111.
                                                                                                                                       receptor-dependent clearance; receptor-independent clearance;
haemophilia; half-life; ss.
                                     30-NOV-2000
                                                                      WO200071714-A2
                                                                                                      Homo sapiens.
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24-MAY-1999;

99US-0135847

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in the bloodstream. The A2 domain mutants exhibit reduced LRP-dependent (receptor-dependent) clearance of factor VIII, while C2 domain mutants have reduced receptor-independent clearance. The invention also relates to a method of using RAP (receptor associated protein), a protein which inhibits LRP (low density lipoprotein related protein)-mediated ligand internalisation, to increase the half-life of factor VIII. The mutant factor VIII proteins, and nucleotides encoding them, are useful to rreating haemophilia. RAP, LRP-binding RAP mutants or fragments, and nucleic acids encoding them may also be used in the treatment of the invention. The invention with a mutant factor VIII protein or DNA of the invention. The invention provides means of increasing the half-life of factor VIII by reducing its clearance from plasma. The present
                                                                                                                                                                                                                                                                                                                                              The invention relates to human factor VIII mutants comprising an amino acid substitution at one or more positions in the A2 domain and/or an amino acid substitution at one or more positions in the C2 domain. The invention also encompasses a factor VIII mutant which lacks a domain (AAB46842). The factor VIII mutants have an increased half-life
                                      sequence represents cDNA encoding human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 41; Page 86-101; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Factor VIII mutants having increased half-life useful for treating hemophilia, comprise one or more amino acid substitutions in the A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2 domain of factor VIII -
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Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;

Score 790; DB 22; Length 8967; Pred. No. 3.6e-236;

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT

o Car	FEATURES			COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	ORGANISM	KEYWORDS SOURCE	ACCESSION VERSION	BG700655 LOCUS DEFINITION
/organism="Homo sapiens" /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IHAGE:4815208" /clone_lib="NHLMGC_95" /tissue_type="hippocampus"	Plate: LLAMIO/11 row: 0 Column: 1/ High quality sequence stop: 690. Location/Qualifiers 1 692	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	cDNA Library Preparation: Michael J. Brownstein (NHGKI), SHIIGKI Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	National Institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)	1 (bases 1 to 692) NIH-MGC http://mgc.nci.nih.gov/.	Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	EST.	BG700655.1 GI:13970214	BG7700655 692 bp mRNA EST 07-MAY-2001 602682272F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4815208 5',

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N DKFZp313G1439_r1 313 (synonym: hl.

DKFZp313G1439 5', mRNA sequence.

AL601022

AL601022.1 GI:15164528

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This is the 5' sequence of the clone insert
Clone from S. Wlemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No s1 sequence available. This clone (DKFZp313G1439) is available at the RZPD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequenced by Qiagen (Hilden/Germany) within the cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duesterhoeft, A., Lauber, J.,
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   Charlottenburg, GERMANY; Email: clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2:
cDNA-collection"
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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clone@rzpd.de.
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ATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAA 271
                                                                                                                                                                                                                                                                          atggagttgatgggctgtgatttaaatagttgcagcatgccattgggaatggagagtaaa 340
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                                                                                  aataatocaaaagagtggctgcaagtggacttccagaagacaatgaaagtcacaggagta
                                                                AATAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTA
                                                                                                                                TCTCCTTCAAAAGCTCGACTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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1 (bases 1 to 815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics Laboratory
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/note="Vector: pME18SFL3
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/clone_lib="PLACE1"
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institutes of Health, Mammalian Gene
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 %b. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 241 c 210 g 240 t
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/clone="IMAGE:4915634"
/clone_lib="NCI_CGAP_Brn67"
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Tel: 301 443 170
Fax: 301 443 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE650938 482 bp mRNA EST 06-SEP-2000 UI-M-BH3-asm-g-04-0-UI.rl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-asm-g-04-0-UI 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction: two approaches to facilitate gene
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/Clone="UI-M-BH3-asm-g-04-0-UI"
/Clone_lib="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 ggcaatgtggattcatctgggattaaaacacaatattttttaaccctccaattattgctcga 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGCAATGTGGACTCATCTGGGATTAAGCATAATAGTTTTTAATCCTCCAATTATTGCTCGA 120
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                                                                 .W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
                                                                                                                                                                                                                                                                                    AV748467 NPC Homo sapiens cDNA clone NPCAXA05
AV748467
AV748467.1 GI:10906315
                           Unpublished (2000)
Contact: Qinghua Z
                                                                                                                        Song, H., Peng, Y., Gu, Y., Yang, Y., Qian, B., Liu, F., Qu, J., Gao, X., C
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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89.2%;
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Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mbshi@ms.stn.sh.cn
    chicken.
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                         BI067808 639 bp mRNA.

BST

pgfin.pk008.h22 normalized chitken fat cDNA library Gallus gallus cDNA clone pgfin.pk008.h22 5' similar to gi|6679733

ref|NP_032003.1| coagulation factor VIII; Factor VIII (Mus musculus splQ66194|FA8_MOUSE COAGULATION FACTOR VIII PRECURSOR (PROCOAGULANT COMPONENT) pir|A47004 coagulation factor VIII precursor couse gb|AAA37385.1| (L05573) coagulati, mRNA sequence.
Phasianinae; Gallus.
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/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                       ctagacccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccag
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                                                                                                                                           aatggcaaagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactct 679
                                                                                                                                                                                                                                                      ATTGCCCTGNNGNTAGAGTNNNNNNNCTGNNA
                          attgccctgaggatggaggttctgggctgcga 771
                                                            CTGGAGCCNNCGCTCTTTGCCCCGCTATGTGAGGATACATCCCCGCCACTGGCACAACCAC
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Contact: Larry A. Cogburn
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Cogburn,L.A., Morgan,R.W. and Burnside,J.
Chicken ESTs from fat
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Fax: 302-831-2822
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: pSPORT1"
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/clone_lib="normalized chicken
/sex="Male and Female"
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/db_xref="taxon:9031"
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242 ATTGCTCTGAGGCTTGAGATTCTAGGATGTGAGGCCCAGCAGCAATACTGA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 acaatgaaagtcacaggagtaactactcagggagtaaaatctctgcttaccagcatgtat 559
                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GTGAAAGAGTTCCTTATTTCCAGCAGTCAAGATGGCCATCACTGGACTCAAATTTTATAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ACAATGAAAGTCACTGGAATAATAACCCAGGGAGTGAAATCTCTCTTTACCAGCATGTTT 61
                                                                                                                                                                                                  ctagacccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccag 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , complete (MOUSE);, mRNA sequence. BE847128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE847128 401 bp mRNA EST 26-SEP-2000 uw22bil.yl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3417405 5' similar to gb:L05573' Mus domesticus coagulation factor VIII mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

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/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:3417405"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares mouse 3NbMS"
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 217.4; DB 11; Length 401; Pred. No. 3.5e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW489638 444 bp mRNA EST 24-FEB-2000 UI-M-BH3-asm-g-04-0-UI.Sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-asm-g-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97044477
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//lab_host="Nota" privile Technologies)"
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/dev_stage="27-32 days"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aactctctagacccaccgttactgactcgctaccttcgaattcacccccagagttgggtg 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTCTCTAGACCCACCATTACTCACTCGCTATCTTCGAATTCACCCCCAGATCTGGGAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCAAATTGCTCTGAGGCTTGAGATTCTAGGATGTGAGGCCCAGCAGCAATACTGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTTTGTGAAAGAGTTCCTTATTTCCAGCAGTCAAGATGGCCCATCACTGGACTCAAATT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mt93e12.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:637486 5' similar to gb.105573 Mus domesticus coagulation factor VIII mRNA complete (MOUSE); mRNA sequence.

AA184901 AA184901.1 GI:1,68759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 265)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubumarra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA184901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa. Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                      Email: mouseest@Watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                               MGI:389478
                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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                                                                                                                                           primer: -28M13 rev2 from Amersham
                                                                                                                    quality sequence stop: 250.
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TAG_TISSUE=brain-stems
TAG_SEQ=TCATG"
                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.1%; Score 201.4; DB 10; Length 444;
82.5%; Pred. No. 1.9e-48;
stive 0; Mismatches 46; Indels 6;
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                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 agaagacaatgaaagtcacaggagtaactactcagggagtaaaaatctctgcttaccagca 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAGACAATGAAAGTCACTGGAATAATAACCCCAGGGAGTGAAATCTCTCTTTACCAGCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggagtaatgcctggagacctcaggtgaataatccaaaagagtggctgcaagtggacttcc 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATACAATGGCAAGGTAAAGGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTTGTGAAAGAGTTCCTTATTTCCAGCAGTCAAGATGGCCCATCACTGGACTCAAATTT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACTAATGCCTGGCGACCTCAGGTGAATGATCCAAAACAATGGTTGCAAGT-GACTTAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226;
                                                                                                   Unpublished (1997)
Other_ESTs: uw22b11.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                     BE852200 384 bp mRNA EST 26-SEP-2000 uw22bl1.xl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3417405 imilar to SW:FA8_MOUSE Q06194 COAGULATION FACTOR VIII PRECURSOR
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 384)
                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                  BE852200.1 GI:10310464
                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:637486"
/clone_lib="Soares mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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/organism="Mus musculus"
                               ocation/Qualifiers
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Pred. No. 2.5e-46;
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/strain="C57BL/6J"

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REFERENCE
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AW446518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCCATCACTGGACTCAAATTTTATACAATGGCAAGGTAAAGGTTTTTCAGGGGAATCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tggccatcagtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatca 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218;
                                                                                                                                                                                              1 (bases 1 to 247)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW446518 247 bp
86227 MARC 1BOV Bos 1
AW446518
USDA, ARS, US Medt. Animal Re
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                        Contact: Smith TPL
                                                                                                                 21180013
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                           AW446518.1 GI:6988305
EST.
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                                                                                                                                Res. 11 (4), 626-630 (2001)
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3 c 91 g 110 t
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/lab_host="DH10B"
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/clone="IMAGE:3417405"
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84.2%;
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Pred. No. 4.2
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                                                               Research Center
                                          68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                 Pecora; Bovoidea;
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 tcgctaccttcgaattcacccccagagttgggtgcaccagattgccctgaggatggaggt 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 tcagggaaatcaagactccttcacacctgtggtgaactctctagacccaccgttactgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               760 tctggg 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CCGCTTCCTTCGGATTCACCCGCGGAGCTGGGCGCACCATATCGCCCTGAGGCTGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CAGTAGTCAAGATGGCCATAACTGGACTCCATTTCTTCAGAATGGCAAAGTGAAGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagcagtcaagatggccatcagtggactctcttttttcagaatggcaaagtaaaggtttt 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGGGAAATCAAGACTCCTTCACCCCCGTGGTGAATGCTCTAGACCCCCCGCTGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW456831
AW456831.1
EST.
               20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 431)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                              AW456831 431 bp mRNA EST UI-M-BH3-aqw-h-12-0-UI.S1 NIH_BMAP_M_S4 Mus UI-M-BH3-aqw-h-12-0-UI 3', mRNA sequence.
                                                 20892-9643,
                                                                                                                                                                                                                                                 Mus musculus
                                                               6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                  National Institute of Mental Health
                                                                                                 Contact: Chin, H
                                                                                                                                                   discovery
                                                                                                                                                                Normalization and
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 48 row: F column: 20 Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: xba1; Site_2: xho1;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
68 c 61 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                  GI:7027048
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                                                                                                                                                                subtraction: two
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Pred. No. 4.2e-46;
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                                                                                                                                                               approaches
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                                                                                                                                                                                                                                                                                                                                                musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 247;
                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                  CDNA
                                                                                                                                                                                                                Murinae;
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BASE COUNT
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Best Local Similarity
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                                                    aagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactctctagacc 686
                                                                                                                                                                                                                                                       agttcctcatctccagcagtcaagatggccatcagtggactctcttttttcagaatggca 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTCCTTATTTCCAGCAGTCAAGATGGCCATCACTGGACTCAAATTTTATACAATGGC- 311
                                                                                                                                                                                                                                                                                                                                                                                                           AAGTCACTGGAATAATAACCCAGGGAGTGAAATCTCTCTTTACCAGCATGTTTGTGAAAG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYA=Yes
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-AAGGTTTTTCAGGGGAATCAGGACTCATCCACACCTATGATGAATTCTCTAGACC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/clone="Lib-"NH1-BMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/lab_host="Library is a subtracted library of a series,
ultimately derived from ten regions of the mouse brain
/cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglla, pineal gland, striatum,
hipoccampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
/lab generated. The following serially subtracted libraries
/lab were generated in this process: NIH_BMAP_M_S4,
/lab NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1,
/lab NIH_BMAP_M_S3.1, NIH_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  >ORR1B#LTR/MalR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_SEQ=TCATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_TISSUE=brain-stems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_LIB=NIH_BMAP_M_S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH_BMAP_M_S4 library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%;
82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 190; DB 10; Length 4 Pred. No. 4.5e-45; 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
242 CCTACCCTTCGATTGGAACTGCAAGGTTGTGAGGTAAATGGATGTTCCACACCCCTGGGT 301
                     269 agcactcttcgcatggagttgattggtggattttaaatagttgcagcattgccattggga 328
                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747 tgaggatggaggttctgggctgcgaggcacaggacctctactga 790
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                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                              89 cagittatcatcatgtatagictigatgggaagagiggcagacittatcgagggaaattcc 148
                                                                                                                                                                                                                                                                                                                                                                                     29 attattcacggcatcaagacccagggtgcccgtcagaagttctccagcctctacatctct 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                           2 ATAATCACAGGGATCCAGACCCAAGGTGCCAAACACTACCTGAAGTCCTGCTATACCACA 61
                                                                                                               ttaaccctccaaftaftgctcgafacaftccgffffgcacccaacfcaffafagcaffcgc 268
                                                                                                                                                                                                           actggaaccttaatggtcttctttggcaatgtggattcatctgggataaaacacaatatt 208
                                                                                                                                                                                                                                                                      GAGTTCTATGTAGCTTACAGTTCCAACCAGATCAACTGGCAGATCTTCAAAGGGAACAGC
                                                                                     TTTGACCCACCTATTGTGGCTAGATATATTAGGATCTCTCCAACTCGAGCCTATAACAGA 241
                                                                                                                                                                            ACAAGGAATGTGATGTATTTAATGGCAATTCAGATGCCTCTACAATAAAAGAGAATCAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL552613 927 bp mRNA EST 16-FEB-200: AL552613 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI067YG24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 927)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://fulllength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 745)
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GGAATCAAAGTATTGCACTTCGCCTGGAACTCHTTGGCTGTGA
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                                   gggtgcaccagattgccctgaggatggaggttctgggctgcga 771
                                                                                     TGAAGAACTTTTTCAACCCCCCAATCATTTCCAGGTTTATCCGTGTCATTCCTAAAACAT
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GENERAL INFORMATION:
APPLICANT: COUTO, Linda B.
APPLICANT: COLOSI, Peter C.
APPLICANT: COLOSI, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
CURRENT FILE APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER APPLICATION NUMBER: 60/124,994
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
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CURRENT APPLICATION NUMBER: US/09/470,618

CURRENT FILING DATE: 1999-12-29

EARLIER APPLICATION NUMBER: 09/364,862

EARLIER FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER FILING DATE: 1999-03-24

EARLIER FILING DATE: 1999-03-24

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1999-03-20

EARLIER FILING DATE: 1998-10-20
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APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
TITLE OF INVENTION: by Target Cells
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Patent No. 6221349
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APPLICANT: COLDS, Peter C.

APPLICANTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII

TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII

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TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIIII

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Pred. No. 4.3e-310;
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GENERAL INFORMATION:
APPLICANT: CONNell
APPLICANT: Kaleko,
APPLICANT: Smith,
TITLE OF INVENTION:
                                                                                          Sequence 7, Application US/08484891 Patent No. 5935935
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   INVENTION:
                 Connelly, Sheili
Kaleko, Michael
Smith, Theodore
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                           241 tttgcacccaactcattatagcattcgcagcactctttcgcattggagttgatgggctgtga
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nes 793; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/484,891
FILING DATE: 07-JUN-1995
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ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                               INFORMATION FOR SEQ ID NO: *41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4227 GTGGACTCTCTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT 4286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4167 TCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HIGH LEVEL EXPRESSION TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,2
                                                                                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 20-SEP-1996 CLASSIFICATION: 435 *.**
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 gtggactctcttttttcagaatggcaaagtaaaggtttttcaggggaaatcaagactcctt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 tctgcttaccagcatgtaegtgaaggagttcctcatctccagcagtcaagatggccatca 600
                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
CITY: E
STATE:
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatit
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                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                           APPLICATION NUMBER:
                 LENGTH:
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5. 6114148
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 Federal Street
               4670 base pairs•
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HAAS, JURGEN
                                                                                617-428-7045
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                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: C
US-08-717-294-41
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; Sequence 1, Application US/08882083
; Patent No. 5869292
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
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                                                        US-08-882-083-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3893 TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA 3952
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                                                                                                                                                                                                                                                                                 4133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3953 TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT 4012
                                                                                                                4433 CCTCTACTGAGGGTGGCC 4450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaaagagtggct 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 79.0%;
Local Similarity 99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 tcagaagttctccagcctctacatctctcagttttatcatcatgtatagtcttgatgggaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg
                                                                                                                                                                                                                           TCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCA 4252
                                                                                                                                                                                                                                                                                                                                                                                                               gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                                                                                      CCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAGGCACAGGA
                                                                                                                                                                                   ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga 780
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                                                                                                                                         cctctactgactcgagcc 798
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    Mismatches

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Pred. No. 4.4e-255;
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US-08-882-083-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
4591 TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT 4650
                                                             4411 GGATTCATCTGGGATAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG
                                                                                                                                                                                                                                                                  4351
                                                                                                                                                                                                                                                                                                                                4291
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                361 tactgcttcatcctactttaccaatatgtttgccacctggtctcctttcaaaagctcgact 420
                                                                                                                                                                                                                                                                          121 gaagtggcagacttategaggagàttccactggaaccttaatggtcttcttttggcaatgt 180
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                                                                                                                                                                                                                                    181
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                    1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                             99attcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                        GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT 4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                          793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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35..5017
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99.48; Pred. No. 4.6e-255;
9.48; Mismatches 5;
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; LOCATION: US-08-558-107-1
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                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                    FEATURE:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
                                                                                                                                                                   REGISTRATION NUMBER: 33,715
REFERENCE/FOCKET NUMBER: 30,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4831 GTGGACTCTCTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT
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                                                     TOPOLOGY:
                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                            NAME: ISACSON, John P. REGISTRATION NUMBER: 3
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                            NAME/KEY:
                                                                                                                                         TELEFAX: (202)672-5399
TELEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                                             Sequence 1, Application US/09243539 Patent No. 6130203
                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4291
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                                                                                                                                                                                                                                                                                                                                                                        4771
                               TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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 STREET:
                        ADDRESSEE:
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Washington
           3000 K Street, N.W., Suite 500
                                                                      VOORBERG, Johannes
                       Foley & Lardner
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/243,539
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                        361
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                 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 79.0%; Score 790; DB 3; Length 5035; Local Similarity 99.4%; Pred. No. 4.6e-255;
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                                             TCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAATCCAAAAGAGTGGCT 4710
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LOCATION: 1..6996

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                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                        TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                        FILING DATE: 24-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                  FEATURE:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/276,594A
FILING DATE: 18-JUL_1994
CLASSIFICATION: 435.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JUS 07/950,191
FILING DATE: 24-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELEFAX: \_
TEX: 904136
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MEDIUM TYPE: Floppy disk
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CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                         NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
NAME/KEY: CDS
                              TOPOLOGY:
                                               STRANDEDNESS:
                                                              TYPE:
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                                                              nucleic acid
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RESULT 11
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Best Local Similarity
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hes 790;
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100.0%; Pred. No. 5.8e-255;
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Sequence 1, Application US/08121202 Patent No. 5563045

GENERAL INFORMATION:
APPLICANT: Pittman
APPLICANT: Rehemt

APPLICANT:

Wozney, John M. Rehemtulla, Pittman, Debra

Alnawaz

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CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5195A
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1210 X8574
TELEFAX: (617) 876-5851
FILEFAX: (617) 876-5851
SEQUENCE CHARACTERISTICS:
LENGTH: 7056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 790; Conserva:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                        121
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CITY: Cambridge
STATE: MA
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT
               tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                  TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA 6566
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                                                                   TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT
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                                                                                                                                                  TELEFAX: (619) 452-2616 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   CLASSIFTON:

LIOPPY disk

LIOPPY disk

PC COMPATIBLE

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/366 or FILING DATE:

CLASSIFTON:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 452-1288
                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hsu, David Chi-Tang
APPLICANT: Chang, Steven
TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII
NUMBER OF SEQUENCES: 3
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8967 base pairs
                                     FEATURE:
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APPLICANT:
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                                                   MOLECULE TYPE:
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CITY: Sa
STATE: C
COUNTRY:
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                                                                 TOPOLOGY:
                                                                                   STRANDEDNESS: both
                 NAME/KEY:
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11055 Roselle
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De Polo, Nicolas J.
Hsu, David Chi-Tang
                                                                 unknown
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                                                                                 Sequence 3, Application US/07864004B Patent No. 5364771
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Best Local Similarity
Matches 793; Conserv
                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6616
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                      7156 CCTCTACTGAGGGTGGCC 7173
                                                                                                                                                                                                                                                          7096 CCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAGGCACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Best Local Similarity
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TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cD
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                                                                                                                                                                                                                     6477 TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA
                                                                                                                                                                                                                                                                                          6417 GATCAAGGTGGATCTGTTGGCACCAATGATTATTCACGGCATCAAGACCCAGGGTGCCCG
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ANTI-SENSE:
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CITY: Atlanta
STATE: Georgia
COUNTRY: US
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LOCATION: 5001 . . . 7053
OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 07 APPLICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1 . . . 22//
OTHER INFORMATION: /note= "Equivalent to the Al-A2
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      61 toagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
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                                                                       tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7077
                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864;004
FILING DATE: 07-APR-1992
                               TELEPHONE: 404-815-6367
                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 PG
CITY: Atlanta
STATE: Georgia
COUNTRY: US
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                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
                                                                                   NAME: Pratt, John S. REGISTRATION NUMBER: 29,476
                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                    404-815-6555
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Local Similarity 99.4%;
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LOCATION: 5001 . . . 7053
OTHER INFORMATION: /note= "Equivalent to
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                                               gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaatt
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                                                                                                                                                                                                                                                                                                                                                                     ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                  GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                                                                   TCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAATCCAAAAGAGTGGCT
                                                                                                                                                               tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct
                                                                                                                                                                                                                                                     TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT
                                                                                                                                                                                                                                                                                                                                                        GGATTCATCTGGGATAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG
                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA
GTGGACTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT
           gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 790; DB 1;
Pred. No. 6.8e-255;
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OTHER INFORMATION:

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US-08-212-133A-1
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                                                                                                                                                                                                                                                                                                                              NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31.284
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:".
TELEPHONE: 404-572-6558
TELEPAN: 404-572-6558
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applica Patent No. 5663060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,133A
FILING DATE: March 11, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/864,004
FILING DATE: March 11, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/864,004
FILING DATE: 07-APR41992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L. 1
                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
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                                                      FEATURE:
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                                                                                                                                                 NAME/KEY: Domain LOCATION: 1..2277 OTHER INFORMATION:
                                                                  OTHER INFORMATION:
                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                      TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                  NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
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O Peachtree Street
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/note= "cDNA encoding human
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Best Local Similarity 99.4%;
Matches 793; Conservative
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CCTCTACTGAGGGTGGCC
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Pred. No. 6.8e-255;
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Search completed: January Job time: 12603 sec

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